

Jarrell, Noble

181606

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From: Ramirez, Delia  
Sent: Tuesday, March 07, 2006 5:49 PM  
To: Jarrell, Noble  
Subject: 09/541,462

Hi,

I would like to request the following search:

1. an oligo search (at least 12 nucleotides long) of SEQ ID NO:1 and 2 in the nucleic acid databases (commercial only)

Thank you very much,

---

Delia M. Ramirez, Ph.D.  
Patent Examiner  
Recombinant Enzymes-Art Unit 1652  
USPTO  
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70  
Alexandria, VA 22314  
(571) 272-0938  
delia.ramirez@uspto.gov

Noble  
Fin 3/16/06

4 NNA oligo  
20PR compugen  
20 one

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**Jarrell, Noble**

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**From:** Ramirez, Delia  
**Sent:** Tuesday, March 07, 2006 5:44 PM  
**To:** Jarrell, Noble  
**Subject:** 09/541,462

Hi,

I would like to request the following INTERFERENCE search:

1. SEQ ID NO:1 and 2 in the nucleic acid databases.
2. an oligo search (at least 12 nucleotides long) of SEQ ID NO:1 and 2 in the nucleic acid databases.

Thank you very much,

---

Delia M. Ramirez, Ph.D.  
Patent Examiner  
Recombinant Enzymes-Art Unit 1652  
USPTO  
400 Dulany Street, Remsen Bldg., 2D74, Mail room 2C70  
Alexandria, VA 22314  
(571) 272-0938  
[delia.ramirez@uspto.gov](mailto:delia.ramirez@uspto.gov)

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GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_plus\_P2n model

Run on: March 11, 2006 09:47:22 ; Search time 530 Seconds

(without alignments)

470.166 Million cell updates/sec

Title: US-09-541-462B-2  
 Perfect score: 108  
 Sequence: 1 MAAMDYDTPSGTNSGAGKK.....KTRQVCPFLDNREWEFQKYGH 108

Scoring table: OLIGO  
 Xgapext 60.0 , Xgapext 60.0  
 Ygapext 60.0 , Ygapext 60.0  
 Fgapext 6.0 , Fgapext 7.0  
 DelOp 6.0 , Deletxt 7.0

Searched: 7673375 seqs, 115364844 residues

Word size: 12

Total number of hits satisfying chosen parameters: 12

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-TRANS=human40_cdi -LIST=45 -DOCALIGN=200 -THR SCORE=quality
-ALIGN=15 -MODE=LOCAL -OUTFMT=pcto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=20000000 -HOST=abs06
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-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DBVTIMEOUT=120
-WARN TIMEOUT=10 -THREADES=1 -XGAPOP=60 -XGAPEXT=60 -FGAPPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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Database : Published Applications NA New: \*

- 1: /cgn2\_6/prodata/2/pubpna/us08\_new\_pub.seq:\*
- 2: /cgn2\_6/prodata/2/pubpna/us05\_new\_pub.seq:\*
- 3: /cgn2\_6/prodata/2/pubpna/us07\_new\_pub.seq:\*
- 4: /cgn2\_6/prodata/2/pubpna/pct\_new\_pub.seq:\*
- 5: /cgn2\_6/prodata/2/pubpna/us05\_new\_pub.seq:\*
- 6: /cgn2\_6/prodata/2/pubpna/us09\_new\_pub.seq:\*
- 7: /cgn2\_6/prodata/2/pubpna/us10\_new\_pub.seq:\*
- 8: /cgn2\_6/prodata/2/pubpna/us10\_new\_pub.seq:\*
- 9: /cgn2\_6/prodata/2/pubpna/us11\_new\_pub.seq:\*
- 10: /cgn2\_6/prodata/2/pubpna/us11\_new\_pub.seq:\*
- 11: /cgn2\_6/prodata/2/pubpna/us11\_new\_pub.seq:\*
- 12: /cgn2\_6/prodata/2/pubpna/us11\_new\_pub.seq:\*
- 13: /cgn2\_6/prodata/2/pubpna/us06\_new\_pub.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	68.5	660	9	US-11-096-168A-11809
2	70	64.8	432	9	US-11-096-168A-1405
3	42	38.9	693	9	US-11-096-168A-26820
4	40	37.0	348	9	US-11-096-168A-28569

## ALIGNMENTS

RESULT 1  
 US-11-096-568A-11809  
 ; Sequence 11809, Application US/11096568A  
 ; Publication No. US20060048240A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexandrov, Nickolai et al.  
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptide  
 ; TITLE OF INVENTION: Thereby  
 ; FILE REFERENCE: 2750-1592PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/096,568A  
 ; CURRENT FILING DATE: 2005-04-01  
 ; NUMBER OF SEQ ID NOS: 34471  
 ; SEQ ID NO 11809  
 ; LENGTH: 660  
 ; TYPE: DNA  
 ; ORGANISM: Triticum aestivum  
 ; FEATURE:  
 ; NAME/KEY: misc feature  
 ; LOCATION: (1)-(660)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 13657464  
 US-11-096-568A-11809

Alignment Scores:  
 Pred. No.: 1.49e-71 Length: 660  
 Score: 74.00 Matches: 74  
 Percent Similarity: 100.0% Mismatches: 0  
 Best Local Similarity: 100.0% Indels: 0  
 Query Match: 68.5% Gaps: 0  
 DB: 9

US-09-541-462B-2 (1-108) × US-11-096-568A-11809 (1-660)

Qy 25 LysLysTrpAsnAlaValAlaLeuTrpAlaIleTrpAlaIleTrpAspIleValAlaAsnCysAlaRle 44  
 Db 208 AAGAGTGGACCGGTCTGGCATCTGGTGACACTGGCCTGCATC 267

Qy 45 CysArgAspHisIleMetAspLeuCysIleGluCysGlnAlaAlaSerAlaThr 64  
 Db 268 TGCCTAACACATGGATTATGGATGGTCCAGGCCAACAGGCCAGGCCACC 327

Qy 65 SerGluGluCysIleValAlaIleTrpGlyIleValCysSerHisAlaPheHisPheHisCysIle 84  
 Db 328 AGCGGGAGTCGCACTGGTCTGTTCACTTCACATGCTTCACATGCTAC 387

Qy 85 SerArgTripleLysThrArgGlnValCysProlLeuAspAsn 98  
 Db 388 AGCAGTGGCTAAAGTCGCCAAAGTCGCCATGACAC 429

RESULT 2  
 US-11-096-568A-14405  
 ; Sequence 14405, Application US/11096568A  
 ; Publication No. US20060048240A1  
 ; GENERAL INFORMATION:  
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
 ; TITLE OF INVENTION: Thereby  
 ; FILE REFERENCE: 2750-1592PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/096,568A  
 ; CURRENT FILING DATE: 2005-04-01  
 ; NUMBER OF SEQ ID NOS: 34471  
 ; SEQ ID NO 14405

LENGTH: 432  
 TYPE: DNA  
 ORGANISM: *zea mays* subsp. *mays*  
 FEATURE: misc\_feature  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(432)  
 OTHER INFORMATION: Ceres Seq. ID no. 4776740  
 US-11-096-568A-14405

Alignment Scores:  
 Pred. No.: 2.64e-67 Length: 432  
 Score: 70.00 Matches: 70  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 64.8% Indels: 0  
 DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) × US-11-096-568A-14405 (1-432)

Qy 29 AlavalAlaLeuTrpAlaTrpAspIleValAspAsnCysAlaIleCysArgAsnHis 48  
 Dbs 18B GCGGTCGGCTCTGGGATCTGGATATCGTGTGACATTGCCATCTGGAGAACAC 247

Qy 49 IleMetAspLeuCysIleGluCysGlnAlaLysGlnAlaSerAlaThrSerGluCys 68  
 Db 248 ATCATGGATCTCTGTTGTTGATGTCAGGGTAATCAGGCCAGGCTAACAGTGAGGATGC 307

Qy 69 ThrValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgIle 88  
 Db 308 ACTGTTGCTTGGGGTTGAAATCACGGCTTCACTTCACCTGATCAGAGATGTTA 367

Qy 89 LysThrArgGlnIvaCysProLeuAspAsn 98  
 Db 368 AAAGACTCGTCAAGTTGCCCCATTGGATAAC 397

RESULT 3  
 US-11-096-568A-26820  
 ; Sequence 26820, Application US/11096568A  
 ; Publication No. US20060048240A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexandrov, Nickolai et al.  
 ; TITLE OF INVENTION: Therby  
 ; FILE REFERENCE: 2750-1592PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/096,568A  
 ; CURRENT FILING DATE: 2005-04-01  
 ; NUMBER OF SEQ ID NOS: 34471  
 ; SEQ ID NO: 26820  
 ; LENGTH: 693  
 ; TYPE: DNA  
 ; ORGANISM: *zea mays* subsp. *mays*  
 ; FEATURE: misc\_feature  
 ; LOCATION: (1)..(693)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 13622871  
 US-11-096-568A-26820

Alignment Scores:  
 Pred. No.: 2.29e-36 Length: 693  
 Score: 42.00 Matches: 42  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 38.9% Indels: 0  
 DB: 9

US-09-541-462B-2 (1-108) × US-11-096-568A-26820 (1-693)

Qy 32 LeuTrpAlaTrpAspIleValAspAsnCysAlaIleCysArgAsnHisIleMetAsp 51  
 Db 207 CTCTGGCTCTGGACATCTGTGGCAACTGGCCAAACACATCATGAC 266

RESULT 4  
 US-11-096-568A-28569  
 ; Sequence 28569, Application US/11096568A  
 ; Publication No. US20060048240A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexandrov, Nickolai et al.  
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
 ; FILE REFERENCE: 2750-1592PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/096,568A  
 ; CURRENT FILING DATE: 2005-04-01  
 ; NUMBER OF SEQ ID NOS: 34471  
 ; SEQ ID NO: 28569  
 ; LENGTH: 348  
 ; TYPE: DNA  
 ; ORGANISM: *Arabidopsis thaliana*  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(348)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 3017472  
 US-11-096-568A-28569

Alignment Scores:  
 Pred. No.: 2.07e-34 Length: 348  
 Score: 40.00 Matches: 68  
 Percent Similarity: 97.1% Conservative: 0  
 Best Local Similarity: 97.1% Mismatches: 1  
 Query Match: 37.0% Indels: 2  
 DB: 9 Gaps: 0

US-09-541-462B-2 (1-108) × US-11-096-568A-28569 (1-348)

Qy 29 AlavalAlaLeuTrpAlaTrpAspIleValAspAsnCysAlaIleCysArgAsnHis 48  
 Dbs 106 GCTCTCGTCCTCTGGCTTGGGATCTGGGATACCTGGTGTATACTGGGAATCAC 165

Qy 49 IleMetAspLeuCysIleGluCysGlnAlaLysGlnAlaSerAlaThrSerGluGluCys 68  
 Db 166 ATCATGGATCTCTGTTGAAATGCTCTAGTGGCAACTAGTGGAAATG 224

Qy 68 SerValAlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgIle 88  
 Db 225 CACTGTTCTCTGGGGTTGAAACCACGCCCTTACTCTGATCAGCATGGCT 284

Qy 88 UlvysThrArgGlnValCysProLeuAsp 97  
 Db 285 CAAAACTCTCAAACTGTGTCACATGAT 312

RESULT 5  
 US-10-332-182A-81117/C  
 ; Sequence 81117, Application US/10932182A  
 ; Publication No. US2006004253A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NAKAO, YOSHIIRO  
 ; APPLICANT: NAKAMURA, NORIHISA  
 ; APPLICANT: KODAMA, YUKIKO  
 ; APPLICANT: FUJIMURA, TONAKI  
 ; APPLICANT: ASHIKARI, TOEIHIKO  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 ; FILE REFERENCE: 03085-043  
 ; CURRENT APPLICATION NUMBER: US/10/932,182A  
 ; CURRENT FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO: 81177  
 ; LENGTH: 153  
 ; TYPE: DNA  
 ;

Qy 32 LeuCysIleGluCysGlnAlaLysGlnAlaSerAlaThrSerIleGluCysSerValAla 71  
 Db 207

ORGANISM: *Saccharomyces pastorianus*  
US-10-932-182A-81177

US-10-932-182A-6146

Alignment Scores:  
Pred. No.: 0.000629 Length: 153  
Score: 12.00 Matches: 12  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 11.1% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-81177 (1-153)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50  
Dy ||||| ||||| ||||| ||||| ||||| |||||  
Db 68 GTTGACACTGTGCTATTGGAAACCATATAATG 33

RESULT 6

US-10-932-182A-81177/c  
Sequence 81177, Application US/10932182A  
Publication No. US20060046253A1  
GENERAL INFORMATION:  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHIWA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIKO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: 030685-043  
CURRENT APPLICATION NUMBER: US/10-932-182A  
CURRENT FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO: 81177  
LENGTH: 153  
TYPE: DNA  
ORGANISM: *Saccharomyces pastorianus*  
US-10-932-182A-81177

Alignment Scores:  
Pred. No.: 0.000629 Length: 153  
Score: 12.00 Matches: 12  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 11.1% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-81177 (1-153)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50  
Dy ||||| ||||| ||||| ||||| |||||  
Db 68 GTTGACACTGTGCTATTGGAAACCATATAATG 33

RESULT 7

US-10-932-182A-6146/c  
Sequence 6146, Application US/10932182A  
Publication No. US20060046253A1  
GENERAL INFORMATION:  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHIWA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIKO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: 030685-043  
CURRENT APPLICATION NUMBER: US/10-932-182A  
CURRENT FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO: 6146  
LENGTH: 207  
TYPE: DNA  
ORGANISM: *Saccharomyces pastorianus*  
US-10-932-182A-6146

Alignment Scores:  
Pred. No.: 0.000629 Length: 153  
Score: 12.00 Matches: 12  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 11.1% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-6146 (1-207)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50  
Dy ||||| ||||| ||||| |||||  
Db 47 GTTGACACTGTGCTATTGGAAACCATATAATG 12

RESULT 8

US-10-932-182A-6146/c  
Sequence 6146, Application US/10932182A  
Publication No. US20060046253A1  
GENERAL INFORMATION:  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHIWA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIKO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: 030685-043  
CURRENT APPLICATION NUMBER: US/10-932-182A  
CURRENT FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO: 6146  
LENGTH: 207  
TYPE: DNA  
ORGANISM: *Saccharomyces pastorianus*  
US-10-932-182A-6146

Alignment Scores:  
Pred. No.: 0.000629 Length: 153  
Score: 12.00 Matches: 12  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 11.1% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-6146 (1-207)

Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50  
Dy ||||| ||||| |||||  
Db 47 GTTGACACTGTGCTATTGGAAACCATATAATG 12

RESULT 9

US-10-932-182A-2279  
Sequence 2279, Application US/10932182A  
Publication No. US20060046253A1  
GENERAL INFORMATION:  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHIWA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIKO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: 030685-043  
CURRENT APPLICATION NUMBER: US/10-932-182A  
CURRENT FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO: 2279  
LENGTH: 366  
TYPE: DNA  
ORGANISM: *Saccharomyces pastorianus*  
US-10-932-182A-2279

```

Alignment Scores:
Pred. No.: 0.00128 Length: 366
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-2279 (1-366)
Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 154 GTTGACAACGTGCTTATTCAGAACCATATA 189

```

```

Alignment Scores:
Pred. No.: 0.00128 Length: 366
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-2279 (1-366)
Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 154 GTTGACAACGTGCTTATTCAGAACCATATA 189

```

```

Alignment Scores:
Pred. No.: 0.00128 Length: 366
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-2279 (1-366)
Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 154 GTTGACAACGTGCTTATTCAGAACCATATA 189

RESULT 12
US-10-932-182A-78459
; Sequence 78459, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO: 78459
; LENGTH: 366
; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-78459

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```

Alignment Scores:
Pred. No.: 0.00128 Length: 366
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-78459 (1-366)
Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 154 GTTGACAACGTGCTTATTCAGAACCATATA 189

```

```

Alignment Scores:
Pred. No.: 0.00128 Length: 366
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-78459 (1-366)
Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 154 GTTGACAACGTGCTTATTCAGAACCATATA 189

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Alignment Scores:
Pred. No.: 0.00128 Length: 366
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-932-182A-78459 (1-366)
Qy 39 ValAspAsnCysAlaIleCysArgAsnHisIleMet 50
Db 154 GTTGACAACGTGCTTATTCAGAACCATATA 189

Search completed: March 11, 2006, 12:07:37
Job time : 531 secs

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OM protein - nucleic search, using frame\_plus\_P2n model

Run on: March 11, 2006, 08:24:33 ; Search time 653 Seconds  
(without alignments)

Scoring table: BLOSUM62

Title:	US-09-541-462B-2
Perfect score:	616
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Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-Q=/abs/ANSWER_spool/US0954162/runat_10032006_080735_22137/app_query.fasta_1
-DB=Published_Applications_NA_Main -QFMT=fastap -SUFFIX=rnpbm -MINMATCH=0.1
-LOOPCH=0 -LOOPEXT=0 -UNITS=bits -START=-1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdd -LIST=45 -DOCALIGN=200 -THR=SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFORMAT=pto -NORMnext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=2000000 -HOST=absbs0h
-USER=US09541462 @CGN_1_1_1026 @runat_10032006_080735_22137 -NCPU=6 -ICPU=3
-NO_MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=10 -LONGLOG -DEVTIMOUT=120
-WARN TIMEOUT=30 -THEADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DLOBP=6 -DELEXT=7

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Database :

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1: /cgn2_6/picode/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/picode/1/pubpna/US08_PUBCOMB.seq:*
3: /cgn2_6/picode/1/pubpna/US09A_PUBCOMB.seq:*
4: /cgn2_6/picode/1/pubpna/US09B_PUBCOMB.seq:*
5: /cgn2_6/picode/1/pubpna/US10A_PUBCOMB.seq:*
6: /cgn2_6/picode/1/pubpna/US10B_PUBCOMB.seq:*
7: /cgn2_6/picode/1/pubpna/US10C_PUBCOMB.seq:*
8: /cgn2_6/picode/1/pubpna/US10D_PUBCOMB.seq:*
9: /cgn2_6/picode/1/pubpna/US10E_PUBCOMB.seq:*
10: /cgn2_6/picode/1/pubpna/US11_PUBCOMB.seq:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	616	100.0	433	7 US-10-242-535A-43377	Sequence 43377, A
2	616	100.0	433	7 US-10-085-783A-43377	Sequence 43377, A
3	616	100.0	453	7 US-10-242-535A-35025	Sequence 35025, A
4	616	100.0	453	7 US-10-085-783A-35025	Sequence 35025, A
5	616	100.0	467	7 US-10-242-535A-35933	Sequence 35933, A
6	616	100.0	467	7 US-10-085-783A-35933	Sequence 35933, A
7	616	100.0	471	7 US-10-242-535A-57254	Sequence 57254, A

## ALIGNMENTS

RESULT 1  
US-10-242-535A-43377  
; Sequence 43377, Application US/10242535A  
; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; ATTORNEY OR AGENT NAME: Lieuw, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10-242-535A  
; CURRENT FILING DATE: 2002-09-12  
; PRIORITY FILING NUMBER: US 10/085-783  
; PRIORITY FILING DATE: 2002-02-28  
; PRIORITY APPLICATION NUMBER: US 60/305,340  
; PRIORITY FILING DATE: 2001-07-13  
; PRIORITY APPLICATION NUMBER: US 60/275,017  
; PRIORITY FILING DATE: 2001-03-12  
; PRIORITY APPLICATION NUMBER: US 60/271,955  
; PRIORITY FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: Patentin version 3.2  
; SEQ ID NO: 43377  
; LENGTH: 433  
; TYPE: DNA  
; ORGANISM: Human  
US-10-242-535A-43377

Length: 433  
Matches: 108  
Conservative: 0

Score: 616.00  
Percent Similarity: 100.0%

Best Local Similarity: 100.0%  
 Query Match: 100.0%  
 DB: 7

US-09-541-462B-2 (1-108) x US-10-242-535A-43377 (1-433)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20  
 Db 20 ArgGCGCAGGGATCATGTGATAACGCCAGCACCACAGGGGGAAAGAG 79

Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAsp 40  
 Db 80 CGCTTGAAGTGAAGTGAAGAAAAGTCGAAATCGAGCCCTCTGGCTGGATATTGTGTTGAT 139

Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60  
 Db 140 AACTGCCCCATCTGAGAACCATTTGCTAGATGTCAGCTAACGTAACCG 199

RESULT 3  
 US-10-242-535A-35025  
 ; Sequence 35025, Application US/10242535A  
 ; Publication No. US20040013663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2005  
 ; CURRENT APPLICATION NUMBER: US/10/242,535A  
 ; CURRENT FILING DATE: 2002-09-12  
 ; PRIORITY APPLICATION NUMBER: US 10/085,783  
 ; PRIORITY FILING DATE: 2002-02-28  
 ; PRIORITY APPLICATION NUMBER: US 60/306,340  
 ; PRIORITY FILING DATE: 2001-07-13  
 ; PRIORITY APPLICATION NUMBER: US 60/275,017  
 ; PRIORITY FILING DATE: 2001-03-12  
 ; PRIORITY APPLICATION NUMBER: US 60/271,955  
 ; PRIORITY FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: Patentin version 3.2  
 ; SEQ ID NO: 35025

Alignment Scores:  
 Pred. No.: 2.89e-74  
 Score: 616.00  
 Percent Similarity: 100.0%  
 Best Local Similarity: 100.0%  
 Query Match: 100.0%  
 DB: 7

US-09-541-462B-2 (1-108) x US-10-242-535A-35025 (1-433)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyAlaGlyLys 20  
 Db 24 ATGGCGCAGGGATCATGTGATAACGCCCTGGATACCCAGGCGCACAAAGGGCAAGAAG 83

21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAsp 40  
 84 CGCTTGAAGTGAAGTGAAGAAAAGTCGAAATCGAGCCCTGGATATGTGTTGAT 143

41 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60  
 144 AACATGCCATCTGGAGACCAATTGGATAGTGTCAAATGGTCAAGCTAACCG 203

US-09-541-462B-2 (1-108) x US-10-085-783A-43377 (1-433)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20  
 Db 20 ATGGCGCAGGGATCATGTGATAACGCCCTGGATACCCAGGCGCACAAAGGGCAAGAAG 79

21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAsp 40  
 80 CGCTTGAAGTGAAGTGAAGAAAAGTCGATCTGGCTGGATATGTGTTGAT 139

Oy 101 TrpGlutpheGlnLysTrgLyHis 108  
 ||||| ||||| |||||  
 Db 324 TGGAAATCCAAAGTATGGCAC 347

RESULT 4  
 US 10-085-783A-35025  
 ; Sequence 35025, Application US/10085783A  
 ; Publication No. US20040037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Chondrodene Inc.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US/10/085,783A  
 ; CURRENT FILING DATE: 2002-02-28  
 ; PRIORITY NUMBER: US 60/305,340  
 ; PRIORITY FILING DATE: 2001-07-13  
 ; PRIORITY APPLICATION NUMBER: US 60/275,017  
 ; PRIORITY FILING DATE: 2001-03-12  
 ; PRIORITY APPLICATION NUMBER: US 60/271,955  
 ; PRIORITY FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 39933  
 ; LENGTH: 467  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-242-535A-39933

Alignment Scores:  
 Pred. No.: 3.01e-74 Length: 467  
 Score: 616.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-39933 (1-467)

Oy 1 MetAlaAlaAlaMetAspThrProserGlyThrAsnSerGlyAlaGlyLysLys 20  
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 Db 20 ATGGCGCAGGCCATGGATGTGGATAACCCGAGGCCAACAGGCAGGCCAGAG 79

Alignment Scores:  
 Pred. No.: 2.89e-74 Length: 453  
 Score: 616.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-35025 (1-453)

Oy 1 MetAlaAlaAlaMetAspAlaAspThrProserGlyThrAsnSerGlyAlaGlyLys 20  
 ||||| ||||| |||||  
 Db 24 ATGGCGCAGGCCATGGATGTGGATAACCCGAGGCCAACAGGCAGGCCAGAG 83

Oy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40  
 ||||| ||||| |||||  
 Db 80 CGCTTGAAAGGAAGAAAGTGGATATGGCTCTGGGCTGGATATGGCTGTGAT 139

Oy 41 AsnCysAlaLysCysArgAsnHsileMetAspLeucysIleGluCysGlnAlaAsnGln 60  
 ||||| ||||| |||||  
 Db 140 AACGTGCCATCTGGAAACCACATATGGATCTTGCATAAGATGTCAGCTAACACAG 199

Oy 61 AlaSerAlaLysSerGluGluCysSerValAlaTrpGlyValCysAsnHsileAlaPheHis 80  
 ||||| ||||| |||||  
 Db 200 GGTGCGCTACTTCAGAGACTGTACGAGACTGTACCTGGCATGGCTTCAC 259

Oy 81 PheHisCysIleSerIgTrpLeuLysThrArgGlnValCysProleuAspAsnArgGlu 100  
 ||||| ||||| |||||  
 Db 260 TTCACTGCATCTCTGCTGCTCAAACACGAGCTCATGGACAAACAGAG 319

Oy 101 TrpGlutpheGlnLysTrgLyHis 108  
 ||||| |||||  
 Db 320 TGGAAATTCCAAAAGATGGCAC 343

RESULT 6  
 US-10-085-783A-39933  
 ; Sequence 39933, Application US/10085783A  
 ; Publication No. US20040037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; C. C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US/10/085,783A  
 ; CURRENT FILING DATE: 2002-02-28  
 ; PRIORITY APPLICATION NUMBER: US 60/305,340  
 ; PRIORITY FILING DATE: 2001-07-13  
 ; PRIORITY APPLICATION NUMBER: US 60/275,017  
 ; PRIORITY FILING DATE: 2001-03-12  
 ; PRIORITY APPLICATION NUMBER: US 60/271,955  
 ; PRIORITY FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 39933  
 ; LENGTH: 467  
 ; TYPE: DNA

ORGANISM: Human  
US-10-085-783A-39933

Alignment Scores:  
Pred. No.: 3.01e-74 Length: 467  
Score: 616.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Minmatches: 0  
Query Match: 100.0% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-39933 (1-467)

QY 1 MetAlaAlaAlaValAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20  
Db 17 ATGCCGGAGCCGATGGTGGTACCCGAGGGCAACGGCCAGAAAG 76

QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40  
Db 77 CGCTTGAACTGTAAGTGAAGAAAGTGGAAATGCACTAGCAGTAGCCCTCTGGCTGGATATTGTGTTGAT 136

QY 41 AsnCysAlaIleCysArgAsnHisIleLeuAspIleCysGlnAlaAsnGln 60  
Db 137 AACGTGCCCCATTCAGGACCACATTGGATTTGATAAGATGTCAGCTAACAG 196

QY 61 AlaSerAlaThrSerGluGlyCysThrValAlaTrpGlyValCysSASHisAlaPheHis 80  
Db 197 GCGTCGGTACTCAGAAGCTGACTGCACTGGAAATGGCTTCAC 256

QY 81 PheHisCysIleSerArgTrpLeuLysThrArgInValCysProLeuAspAsnArgGlu 100  
Db 257 TTCCACTGCATCTCGTGGCTCAAAACGAGAACTGGACAGAGAG 316

QY 101 TrpGluPheGlnLysLysTrpGlyHis 108  
Db 317 TGGAAATTCCAAGAATGGCAC 340

RESULT 8  
US-10-085-783A-57254  
; Sequence 57254, Application US/10085783A  
; Publication No. US20040037841A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; ATTORNEY: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2002  
; CURRENT APPLICATION NUMBER: US/10/085,783A  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 57254  
; LENGTH: 471  
; TYPE: DNA  
; ORGANISM: Human  
; APPLICANT: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10244235A  
; PRIOR APPLICATION NUMBER: US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; ATTORNEY: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; PRIOR APPLICATION NUMBER: US-10-085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 57254  
; LENGTH: 471  
; TYPE: DNA  
; ORGANISM: Human  
; US-10-242-535A-57254

Alignment Scores:  
Pred. No.: 3.05e-74 Length: 471  
Score: 616.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Minmatches: 0  
Query Match: 100.0% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-57254 (1-471)

QY 1 MetAlaAlaAlaMetAspValAspThrProSerGlyAlaGlyLysLys 20  
Db 17 ATGCCGGCAGGGATGGCTGGCTGGCTGGATATTGTGTTGAT 136

QY 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40  
Db 77 CGCTTGAACTGTAAGTGAAGAAAGTGGAAATGCACTAGCAGTAGCCCTCTGGCTGGATATTGTGTTGAT 136

QY 41 AsnCysAlaIleCysArgAsnHisIleMetAspIleCysIleGluCysGlnAlaAsnGln 60  
Db 137 AACGTGCCCCATTCAGGACCACATTGGATTTGATAAGATGTCAGCTAACAG 196

QY 61 AlaSerAlaThrSerGluGlyCysThrValAlaTrpGlyValCysSASHisAlaPheHis 80





PRIOR APPLICATION NUMBER: US 60/305,340  
*i* PRIORITY FILING DATE: 2001-07-13  
*i* PRIORITY APPLICATION NUMBER: US 60/275,017  
*i* PRIORITY APPLICATION NUMBER: 2001-03-12  
*i* PRIORITY FILING DATE: 2001-02-18  
*i* PRIORITY FILING DATE: 2001-02-18  
*i* NUMBER OF SEQ ID NOS: 58994  
*i* SOFTWARE: PatentIn version 3.2  
*i* SEQ ID NO: 46292  
*i* LENGTH: 523  
*i* TYPE: DNA  
*i* ORGANISM: Human  
*i* US-10-242-535A-46292

Alignment Scores:  
Pred. No.: 3.52e-74 Length: 523  
Score: 616.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) × US-10-085-783A-46292 (1-523)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20  
Db 19 ATGCCGCAGGGATGCGATTCACCCGAGCCACAAAGCGCCGCCGCAAGAACAG 78

Qy 21 ArgPheGluValLysTrpAsnAlaValAlaLeutrpAlaIleAspIleLeuValAsp 40  
Db 79 CGCTTGAAAGTGAAGAAAGTGAATGAACTGGATATTGGGATATTGTGGTTGAT 138

Qy 41 AsnCysAlaLysCysArgAsnHisIleMetAspIleCysGlnAlaLysGln 60  
Db 139 AACTRGccATCTGGAAACCAATTGCTCATAGTCAAGTAACTGGTACAGTACCG 198

Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaIleTrpGlyValCysAsnHisAlaPheHis 80  
Db 199 GCGTCGCCTACTTCGAAGAGTGACTGTGCGATGGGGACTCTGTAACCATGCTTTAC 258

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
Db 259 TTCCACTGCATCTCTGCTGCTCAAACACGACAGGTGTGTCATTGGACAACAGAGAC 318

Qy 101 TrpGluPheGlnLysTrpGlyHis 108  
Db 319 TGGAAATCCAAAAGTAGTGGCAC 342

RESULT 14 US-09-918-995-17191  
*i* Sequence 17191, Application US/09918995  
*i* Publication No. US20030073623A1  
*i* GENERAL INFORMATION:  
*i* APPLICANT: Hyseq, Inc.  
*i* TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
*i* FROM VARIOUS cDNA LIBRARIES  
*i* FILE REFERENCE: 20411-756  
*i* CURRENT APPLICATION NUMBER: US/09/918,995  
*i* CURRENT FILING DATE: 2001-07-30  
*i* PRIOR APPLICATION NUMBER: US/09/235,076  
*i* NUMBER OF SEQ ID NOS: 38054  
*i* SOFTWARE: Fastseq For Windows Version 3.0  
*i* SEQ ID NO: 17191  
*i* LENGTH: 476  
*i* TYPE: DNA  
*i* ORGANISM: Homo sapiens  
*i* FEATURE:  
*i* NAME/KEY: misc\_feature  
*i* LOCATION: (1) ..(476)  
*i* OTHER INFORMATION: n = A,T,C or G

US-09-541-462B-2 (1-108) × US-09-918-995-17191 (1-476)

Qy 2 AlaAlaAlaMetAspValAspThrProSerGlyLysSerGlyAlaGlyLysLys 21  
Db 75 GCGCCAGCGATGGATGGATGGTCATAACCCGAGGGCACCAACAGCGCCGAAAGGCC 134

US-10-085-783A-46292  
*i* Sequence 46292, Application US/10085783A  
*i* GENERAL INFORMATION:  
*i* APPLICANT: ChondroGene Inc.  
*i* APPLICANT: Liew, C.C.  
*i* TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
*i* FILE REFERENCE: 4231/2002  
*i* CURRENT APPLICATION NUMBER: US/10/085,783A  
*i* CURRENT FILING DATE: 2002-02-28  
*i* PRIOR APPLICATION NUMBER: US 60/305,340  
*i* PRIOR FILING DATE: 2001-07-13  
*i* PRIOR APPLICATION NUMBER: US 60/275,017  
*i* PRIOR FILING DATE: 2001-03-12  
*i* PRIOR APPLICATION NUMBER: US 60/271,955  
*i* NUMBER OF SEQ ID NOS: 58994  
*i* SOFTWARE: PatentIn version 3.2  
*i* SEQ ID NO: 46292  
*i* LENGTH: 523  
*i* TYPE: DNA  
*i* ORGANISM: Human  
*i* US-10-085-783A-46292

Qy	22	PheGluValLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAspAsn	41
Db	135	TTCGAAGTGAAGAAATGGATGCGTAGCCTGGCATATGGTGATAAC	194
Qy	42	CysAlaLileCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla	61
Db	195	TGTGCCATCTGCAGCAACCACARTATTGGATCTTGCAAGAACGCTAACAGCG	254
Qy	62	SerAlaThrSerGluGlucysSerValAlaIleTrpGlyValCysAsnHisAlaPheHis	81
Db	255	TCCGCTACTCTCAGAGAGCTACTGCTGATGGGAGCTGTAAACCAGCTTTCACTTC	314
Qy	82	HisCysSerArgTripleuLysThrArgGlnValCysProLeuAspAsnArgGluTrp	101
Db	315	CACTGCATCTCTCGTGGCTCAAACACAACAGAGCTGGCATGGACAAACAGAGTGG	374
Qy	102	GluPheGlnLysTrpGlyHis	108
Db	375	GAATTCAAAAGTATGGGCRC	395

Search completed: March 11, 2006, 08:38:02  
 Job time : 656 secs

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OM protein - nucleic search, using frame\_Plus\_P2n model

Run on: March 15, 2006, 08:51:24 ; Search time 2486 Seconds  
 (without alignments)

Perfect score: 108  
 Sequence: 1 MAJAMDVDTPSGTNSGAGKK.....KTRQVCPUDNREWEFQKYGH 108  
 2469.466 Million cell updates/sec

Scoring table: OLIGOPO

Xgapext	60.0	Xgapext	60.0
Ygapext	60.0	Ygapext	60.0
Fgapext	6.0	Fgapext	7.0
DelOp	6.0	Delect	7.0

Searched: 5883141 seqs, 28421725653 residues

Word size: 12

Total number of hits satisfying chosen parameters: 144

Minimum DB seq length: 0  
 Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-MODEL=frame+P2n.model -DEV=x1DP
-O=/abs$ /ABSSWIB $POOP/US9541462/runat_14032006_083243_8686/app_query.fasta_1
-DB=GenEmbl -QFMT=fstab -SUFFIX=xrge -MINMATCH=0.1 -LOOPCFL=0 -LOCPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIXX=oli90 -TRANS:human40_cdi -LIST=15
-DOCAALIGN=200 -THR SCORE:quality -THR MIN=12 -ALIGN=22 -MODE=LOCAL -OUTFMT=pfo
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=absbs0p
-USER=US9541462 @CCN_1_7415 @runat_14032006_083243_8686 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DISPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=10 -THREADS=1 -XGAPOP=60 -XGAPEXT=7 -DELOP=6 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELEXT=7
```

GenCore version 5.1.7  
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OM protein - nucleic search, using frame\_Plus\_P2n model

Run on: March 15, 2006, 08:51:24 ; Search time 2486 Seconds  
 (without alignments)

Perfect score: 108  
 Sequence: 1 MAJAMDVDTPSGTNSGAGKK.....KTRQVCPUDNREWEFQKYGH 108  
 2469.466 Million cell updates/sec

Scoring table: OLIGOPO

Xgapext	60.0	Xgapext	60.0
Ygapext	60.0	Ygapext	60.0
Fgapext	6.0	Fgapext	7.0
DelOp	6.0	Delect	7.0

Searched: 5883141 seqs, 28421725653 residues

Word size: 12

Total number of hits satisfying chosen parameters: 144

Minimum DB seq length: 0  
 Maximum DB seq length: 20000000000

Post-processing: Listing first 45 summaries

Command line parameters:

```
-MODEL=frame+P2n.model -DEV=x1DP
-O=/abs$ /ABSSWIB $POOP/US9541462/runat_14032006_083243_8686/app_query.fasta_1
-DB=GenEmbl -QFMT=fstab -SUFFIX=xrge -MINMATCH=0.1 -LOOPCFL=0 -LOCPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIXX=oli90 -TRANS:human40_cdi -LIST=15
-DOCAALIGN=200 -THR SCORE:quality -THR MIN=12 -ALIGN=22 -MODE=LOCAL -OUTFMT=pfo
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=absbs0p
-USER=US9541462 @CCN_1_7415 @runat_14032006_083243_8686 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DISPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=10 -THREADS=1 -XGAPOP=60 -XGAPEXT=7 -DELOP=6 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELEXT=7
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GenEmbl:\*

- 1: gb\_ba:\*
- 2: gb\_in:\*
- 3: gb\_env:\*
- 4: gb\_cm:\*
- 5: gb\_cv:\*
- 6: gb\_pat:\*
- 7: gb\_ph:\*
- 8: gb\_pr:\*
- 9: gb\_ro:\*
- 10: gb\_sts:\*
- 11: gb\_sy:\*
- 12: gb\_un:\*
- 13: gb\_vl:\*
- 14: gb\_htg:\*
- 15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	108	100.0	327	8	AF142059	AF142059 Homo sapi
2	108	100.0	433	6	CQ698451	CQ698451 Sequence
3	108	100.0	453	6	CQ690099	CQ690099 Sequence

## ALIGNMENTS

RESULT 1  
 AF142059

LOCUS Homo sapiens RING finger protein (ROCL) mRNA, complete cds.

DEFINITION AF142059

ACCESSION AF142059.1

VERSION GI:4809215

KEYWORDS

SOURCE Homo sapiens

ORGANISM Homo sapiens

Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 327)

AUTHORS Ohta,T., Michel,J.J., Schottelius,A.J. and Xiong,Y.

TITLE ROCL, a homolog of APC11, represents a family of cullin partners with an associated ubiquitin ligase activity

JOURNAL Mol. Cell. 3 (4), 535-541 (1999)

PUBLMED 10230407

REFERENCE 2 (bases 1 to 327)

AUTHORS Ohta,T., Michel,J. and Xiong,Y.

TITLE Direct Submission

JOURNAL University of North Carolina at Chapel Hill, Mason Farm Rd. and Manning Dr., Chapel Hill, NC 27599-7295, USA

FEATURES Location/Qualifiers 1..327

Source /organism="Homo sapiens"



Qy	21	ArgPheGluValLysIleTrpAsnAlaLeuTrpAlaTrpAspIleValValAsp	40	Db	260	TTCATCTGCATCTCGTGGCTCAAAACGACAGGGTGCCATTGGACAACAGAGAG	
Qy	84	CGETTGAGTGAAGTGAAGTGAATCGAATCGAGCCTCTGGGATATGTGTTGAT	143	Qy	101	TrpGluPheGlnIysTrpGlyHis	108
Db	41	AsnCysAlaIleCysArgAsnHisIleMetAspIleCysIleGluCysGlnAlaAsnGin	60	Db	320	TGGAAATCCAAAAGATGGGCCAC	343
Qy	144	AACCTGGCCATCTCCAGAACCCACTTATGATCTTGCATAGATGTCAGTAACCG	203	RESULT 5			
Db	61	AlaSerAlaThrSerGluGluCysThrValAlaIleTrpGlyAlcCysGlnAlaAsnGin	80	COT712328	CQ712328	471 bp	DNA
Qy	204	GCCGCCGGTACTCTGAGAGTGACTGCGCATGGGACTCTGTAACCCTGCTTTCAC	263	LOCUS	57254	from Patent WO02070737.	
Db	81	PheHisCysIleSerArgPheLeuIysThrArgGlnValCysProLeuAspAsnArgGlu	100	DEFINITION	COT712328		
Qy	264	TTCACAGATCATCTGCGTGCCTAAACGACAGGTGTCCATTGACAACAGAG	323	ACCESSION	COT712328		
Db	101	TrpGluPheGlnIysTrpGlyHis	108	VERSION	COT712328.1	GI:42273185	
Qy	324	TGGCAATTCCAAAARGTATGGCAC 347		KEYWORDS			
Db	RESULT 4		SOURCE	Homo sapiens (human)			
	CQ695007	CQ695007	ORGANISM	Homo sapiens			
	LOCUS	39933	FEATURES	Location/Qualifiers			
	DEFINITION	Sequence 39933 from Patent WO02070737.					
	VERSION	CQ695007					
	KEYWORDS	CQ695007.1					
	REFERENCE	GI:42240530					
	AUTHORS	Liew C.C., Marshall, W.E. and Zhang, H.					
	TITLE	Compositions and methods relating to osteoarthritis					
	JOURNAL	Patent: WO 02070737-A 39933 12-SEP-2002;					
	FEATURES	Chondrogen Inc. (CA)					
	ORIGIN	Location/Qualifiers					
	source	1..467					
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		/mol_type="unassigned DNA"					
		/db_xref="taxon:9606"					
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	Pred. No.:	2.38e-112	Length:	467	Db	1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys	20
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	Best Local Similarity:	100.0%	Mismatches:	0	Db	Percent Similarity: 100.0%	Conservative: 0
	Query Match:	100.0%	Indels:	0	Db	Best Local Similarity: 100.0%	Mismatches: 0
	DB:	6	Gaps:	0	Db	Query Match: 100.0%	Indels: 0
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	Qy	1	AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGin	60	Qy	1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys	20
	Db	41	CGCTTGGAGATGGATGAGTGAATGGGATACCCGGAGCGCACCACAGCGAACACATATTGGATCTTCATAGAACGTAACCG	196	Db	2 4e-112	Length: 471
	Qy	81	TGCTTGAAAGTCAAAAGTGGATAGCTAGCCCTCTGGCTGGATATTGGTTGAT	136	Db	Score: 108.00	Matches: 108
	Db	81	CGCTTGGAGATGGATGAGTGAATGGGATACCCGGAGCGCACCACAGCGAACACATATTGGATCTTCATAGAACGTAACCG	196	Db	Percent Similarity: 100.0%	Conservative: 0
	Qy	81	ArgPheGluValLysIleTrpAsnAlaValAlaLeuTrpAlaTrpIleValValAsp	40	Db	Score: 108.00	Matches: 108
	Db	77	CGCTTGGAGATGGCTGAAAGTGGATAGCTAGCCCTCTGGCTGGATATTGGTTGAT	136	Db	Percent Similarity: 100.0%	Conservative: 0
	Qy	21	AlaSerAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGin	60	Qy	1 ArgPheGluValLysIleTrpAsnAlaValAlaLeuTrpAlaTrpIleValValAsp	40
	Db	137	AACTGTGCCATCTGCAGAACACATATTGGATCTTCATAGAACGTAACCG	196	Db	2 4e-112	Length: 471
	Qy	61	AlaSerAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGin	60	Db	Score: 108.00	Matches: 108
	Db	197	CGCTTGGCTACTTCAGAAGAGTGTACTGTCGATGGGAGTCGTAACCATGCTTTCAC	256	Db	Percent Similarity: 100.0%	Conservative: 0
	Qy	81	PheHisCysIleSerGlyArgIleValIysTrpArgGlnValCysProLeuAspAsnArgGlu	100	Qy	1 AsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGin	60
	Db	257	TTCATGCACTCTGCTGGCTAAACACAGCAGGTGTCAATTGGACAACGAG	316	Db	2 4e-112	Length: 471
	Qy	101	TrpGluPheGlnIysTrpGlyHis	108	Db	Score: 108.00	Matches: 108
	Db	317	TGGAAATTCCAAAAGATGGCAC	340	Db	Percent Similarity: 100.0%	Conservative: 0
	Qy	101	TrpGluPheGlnIysTrpGlyHis	108	RESULT 6		
	Db	307			COT711142		
	Qy	101	TrpGluPheGlnIysTrpGlyHis	108	LOCUS	CQ711142	
	Db	307			DEFINITION	Sequence 56068 from Patent WO02070737.	
	Qy	101	TrpGluPheGlnIysTrpGlyHis	108	ACCESSION	COT711142	
	Db	307			VERSION	CQ711142.1	
	Qy	101	TrpGluPheGlnIysTrpGlyHis	108	KEYWORDS		
	Db	307			SOURCE		
	Qy	101	TrpGluPheGlnIysTrpGlyHis	108	ORGANISM	Homo sapiens (human)	
	Db	307			COMMENT	Homo sapiens	
	Qy	101	TrpGluPheGlnIysTrpGlyHis	108	Qy		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

1 Liew,C.C., Marshall,W.E. and Zhang,H.  
Composition and methods relating to osteoarthritis  
Patent: WO 02070737-A 56068 12-SEP-2002;  
Chondogene Inc. (CA)

FEATURES source  
Location/Qualifiers  
1. .472  
/organism="Homo sapiens"  
/mol type="unassigned DNA"  
/db\_xref="taxon:9606";

ORIGIN  
US-09-541-462B-2 (1-108) x CQ711142 (1-472)

Alignment Scores:  
Pred. No.: 2.41e-112 Length: 472  
Score: 108.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) x BD027641 (1-482)

Alignment Scores:  
Pred. No.: 2.45e-112 Length: 482  
Score: 108.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indels: 0  
DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) x BD027641 (1-482)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyYAlaGlyLysLys 20  
Db 20 ATGGCGGAGGGATGGATGGATAACCCGAGCGACAAACGGCCAAAGGAG 79

Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAsp 40  
Db 80 CGCTTGAGTGAAAAGTGTAAAGCTAGATGAGTCAGGCCCTGGGATTTGGTGTGAT 139

Qy 41 AsnCysAlaLysCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60  
Db 149 AACCTGCCATCTCGAGAACCACTATTAGTATGATAGATGTAAGCTAACAG 199

Qy 61 AlaSerAlaThrSerGluGluCysthrValAlaLysPheGlyValCysAsnHisAlaPheHis 80  
Db 209 GCGTCCGGTACTCTAGAGAGTGTACTGTCGATGCTGCTTAACCATGCTTTCGC 268

Qy 81 PheHisCysIleSerArgTrpLeuLysTrtArgGlnValCysProLeuAspAspArgGlu 100  
Db 269 TCCACTGATCTCGTGGCTAAACAGACAGGTGTCCATTGGACAACAGAGNG 328

Qy 101 TrpGluPheGlnLysTrtGlyHis 108  
Db 329 TGGGAATTCAAAAGATGGCAC 352

RESULT 8 AX888031  
LOCUS AX888031 482 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 3894 from Patent EP1033401.  
ACCESSION AX888031  
VERSION AX888031.1 GI:40046785  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
COMMENT 1 (bases 1 to 482)  
REFERENCE Edwards,J.B.M., Ducclair,E. and Jordan,J.Y.  
AUTHORS Sequence tag and encoded human protein  
TITLE Sequence tag and encoded human protein  
JOURNAL Patent : JP 2001269182-A 3887 02-OCT-2001;  
GENSET OS Homo sapiens (human)  
PN JP 2001269182-A/3887  
PD 02-OCT-2001  
PF 24-FEB-2000 JP 2000118773  
PR 26-FEB-1999 US 60/122487  
PI JEAN BAPTIST DUMAS MILNE EDWARDS, EIMERIC DUCLAIR, JEAN YVES  
PI JORDAN



Query Match:	100.0%	Indels:	0	Alignment Scores:	2.55e-112	Length:	504	
DB:	6	Gaps:	0	Pred. No.:	108.00	Matches:	108	
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Qy	1	MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys	20	Percent Similarity:	100.0%	Mismatches:	0	
Db	18	ATGGCGCCGCCGATGGATGCCAACACGGGGCAAAACAGGGCGACAAACAGGGCGACAAAGGAG	77	Best Local Similarity:	100.0%	Indels:	0	
Qy	21	ArgPheGluValLysLysTrpAspAlaValAlaLeuTrpAlaTrpAspIleValAsp	40	Query Match:	100.0%	Gaps:	0	
Db	78	CGGTTGAAGTAAAGTGAAATGGAAATTGGGTAT	137	DB:	9	US-09-541-462B-2 (1-108) x AF140599 (1-504)		
Qy	41	AsnCysAlaIleCysArgSerHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln	60	Qy	1	MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys	20	
Db	138	AACGTGCCCCATCTGAGAACCACTATTGATGATCTTGATGATGTCAGGGCAACCAAG	197	Db	18	ATGGCGCCGCCGATGGATGCCAACACGGGGCAAAACAGGGCGACAAAGGAG	77	
Qy	61	AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis	80	Qy	21	ArgPheGluValLysLysTrpAspAlaLeuTrpAlaTrpAspIleValAspIleValAsp	40	
Db	198	GGTCAGTACTCTTCGAAGAGTGTACGGTTGCATGGGAAGTCTCAACCATGCTTTCAT	257	Db	78	CGCTTGAATTAAAAGTGAATGGCCTCTGGCTCTGGACATTGCTGTTGAT	137	
Qy	81	PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu	100	Qy	41	AsnCysAlaIleCysArgAsnHisIleMetAspIleCysIleGluCysGlnAlaAsnGln	60	
Db	258	TTCCACTGATCTCTGATGCTCAAACAGGGCAAGGTGTGCCAGAACAGAGAG	317	Db	138	AACTGTGCCATCTCAGGACCACATTGGATTTGATGATGATGTCAGGGCAACCCAG	197	
Qy	101	TpGluIleGlnIleIleTrpGlyHis	108	Qy	61	AlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis	80	
Db	318	TGGGAGTTCCAGAAGTAGTGGCAT	341	Db	198	GCCAGCTACTCTCGAAGAGTGTACGGTTGCATGGCTTAAACAGGGAGGTTGTCAGAACAGAGAG	317	
RESULT 1.1				Db	318	TGGGAGTTCCAGAAGTAGTGGCAT	341	
AF140599	AF140599	504 bp	mRNA	linear	ROD 11-MAY-1999	Qy	101 TpGluIleGlnIleIleTrpGlyHis	108
LOCUS	AF140599					Db	318 TGGGAGTTCCAGAAGTAGTGGCAT	341
DEFINITION	Mus musculus ring-box protein 1 (Rbx1) mRNA, complete cds.					Qy	101 TpGluIleGlnIleIleTrpGlyHis	108
ACCESSION	AF140599					Db	318 TGGGAGTTCCAGAAGTAGTGGCAT	341
VERSION	AF140599.1					Qy	101 TpGluIleGlnIleIleTrpGlyHis	108
KEYWORDS	Mus musculus (house mouse)					Db	318 TGGGAGTTCCAGAAGTAGTGGCAT	341
SOURCE	Mus musculus					Qy	101 TpGluIleGlnIleIleTrpGlyHis	108
ORGANISM	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;					Db	318 TGGGAGTTCCAGAAGTAGTGGCAT	341
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;					Qy	101 TpGluIleGlnIleIleTrpGlyHis	108
	Sciurognathi; Muroidea; Muridae; Murinae; Mus.					Db	318 TGGGAGTTCCAGAAGTAGTGGCAT	341
REFERENCE	Kamura,T., Koepf,D.M., Conrad,M.N., Skovronyra,D., Moreland,R.J., Iliopoulos,O., Lane,W.S., Kaelin,W.G. Jr., Eledge,S.J., Conaway,R.C., Harper,J.W. and Conaway,J.W.					Qy	101 TpGluIleGlnIleIleTrpGlyHis	108
AUTHORS	Rbx1, a component of the VHL tumor suppressor complex and SCP ubiquitin ligase					Db	318 TGGGAGTTCCAGAAGTAGTGGCAT	341
TITLE	Science 284 (5414), 657-661 (1999)					Qy	101 TpGluIleGlnIleIleTrpGlyHis	108
JOURNAL	10213691					Db	318 TGGGAGTTCCAGAAGTAGTGGCAT	341
PUBLMED	(bases 1 to 504)					Qy	101 TpGluIleGlnIleIleTrpGlyHis	108
REFERENCE	Kamura,T., Lane,W.S., Conaway,R.C. and Conaway,J.W.					Db	318 TGGGAGTTCCAGAAGTAGTGGCAT	341
AUTHORS	Direct Submission					Qy	101 TpGluIleGlnIleIleTrpGlyHis	108
TITLE	Submitted (05-APR-1999) Prog. Molec. Cell. Biol., HHMI, Oklahoma Med. Res. Found., 825 NE 13th St., Oklahoma City, OK 73104, USA					Db	318 TGGGAGTTCCAGAAGTAGTGGCAT	341
JOURNAL	Med. Res. Location/Qualifiers					Qy	101 TpGluIleGlnIleIleTrpGlyHis	108
FEATURES	source					Db	318 TGGGAGTTCCAGAAGTAGTGGCAT	341
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	/db_xref="taxon:10090"					Qy	101 TpGluIleGlnIleIleTrpGlyHis	108
gene	/gene="rbx1"					Db	318 TGGGAGTTCCAGAAGTAGTGGCAT	341
CDS	1..344					Qy	101 TpGluIleGlnIleIleTrpGlyHis	108
	/gene="rbx1"					Db	318 TGGGAGTTCCAGAAGTAGTGGCAT	341
	/note="component of VHL tumor suppressor complex and SCF ubiquitin ligase"					Qy	101 TpGluIleGlnIleIleTrpGlyHis	108
	/codon_start=1					Db	318 TGGGAGTTCCAGAAGTAGTGGCAT	341
	/product="ring-box protein 1"					Qy	101 TpGluIleGlnIleIleTrpGlyHis	108
	/protein_id="P429716.1"					Db	318 TGGGAGTTCCAGAAGTAGTGGCAT	341
	/db_xref="GI:4769006"					Qy	101 TpGluIleGlnIleIleTrpGlyHis	108
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	ORIGIN					Db	318 TGGGAGTTCCAGAAGTAGTGGCAT	341

Db 7 ATGGGCCAGGGATGGATGCGATACCCCAGCCACAGGGCGGCCAAGGAAG 66  
 Qy 21 ArgPheGluValLysIleSTPAsnAlaValAlaLeuTrpAlaTTPAspIleValAsp 40  
 Db 67 CGCTTGAAGGAAAGTGAATGCGATGCCCTGGCTGGATATGTGGTGTAT 126  
 Qy 41 AsnCysAlaLileCysArgAsnIleMetAspLeuCysIleGlucysGlnAlaAsnGln 60  
 Db 127 AACTGTGCCATTCTGAGAACCATATTGATCTTGCAATAAGCTAACAG 186  
 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrrGlyValCysAsnHisAlaPheHis 80  
 Db 187 GCGTCCCTACTTCAGAGAGTGTACTGTCATGGAGACTGTAACCATGCTTTAC 246  
 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 247 TTCCACTGCATCTCGCTCAAACAGACAGGGTGTCTGCATGGAAACAGAGAG 306  
 Qy 101 TrpGluPheGlnLysTyrGlyHis 108  
 Db 307 TGGGAATTCCAAGATGGGAC 330

RESULT 13  
 BD271520 LOCUS VonHippel-Lindau tumor suppressor complex and novel component of PAT 17-JUL-2003  
 DEFINITION SCP ubiquitin ligase. DNA linear PAT 20-APR-2005  
 SOURCE Db 307 TGGGAATTCCAAGATGGGAC 330

ACCESSION AR640603  
 VERSION BD271520\_1 GI:33081288  
 KEYWORDS JP 2002341775-A/1.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Hominidae; Homo.  
 1 (bases 1 to 508) Conaway,J.W., Conway,R.C. and Kamura,T.  
 REFERENCE VonHippel-Lindau tumor suppressor complex and novel component of  
 SCP ubiquitin ligase  
 CONAWAY,J.W., CONWAY,R.C. and KAMURA,T.  
 TITLE Patent: US 2002341775-A 1 10-DEC-2002;  
 OKLAHOMA MEDICAL RESEARCH FOUNDATION  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002341775-A/1  
 PD 10-DEC-2002  
 PF 25-FEB-2000 JP 2000601023  
 PR 26-FEB-1999 US 601211787  
 PI JOAN W CONAWAY, RONALD C CONAWAY, TAKUMI KAMURA, PC  
 C12N15/09, A61K38/00, A61K45/00, A61P35/00, C07K14/47, PC  
 PC C12N1/19, C12N1/21, C12N5/10, C12N9/00, C12P21/02, G01N33/15, G01N33/ PC  
 FT 50, G01N33/68  
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 FT 1. .508  
 PC vonHippel-Lindau tumor suppressor complex and novel component  
 CC of SCP  
 CC ubiquitin ligase  
 FH Key  
 FT source 1. .508  
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 DB: 6 Gaps: 0

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 Qy 21 ArgPheGluValLysIleSTPAsnAlaValAlaLeuTrpAlaTTPAspIleValAsp 40  
 Db 67 CGCTTGAAGGAAAGTGAATGCGATGCCCTGGCTGGATATGTGGTGTAT 126  
 Qy 41 AsnCysAlaLileCysArgAsnIleMetAspLeuCysIleGlucysGlnAlaAsnGln 60  
 Db 127 AACTGTGCCATTCTGAGAACCATATTGATCTTGCAATAAGCTAACAG 186  
 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrrGlyValCysAsnHisAlaPheHis 80  
 Db 187 GCGTCCCTACTTCAGAGAGTGTACTGTCATGGAAACAGAGAG 306  
 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 247 TTCCACTGCATCTCGCTGCCTCAAACAGACAGGGTGTCTGCATGGAAACAGAGAG 306  
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 Db 307 TGGGAATTCCAAGATGGGAC 330

RESULT 14  
 AR640603 LOCUS AR640603 Sequence 3 from patent US 6858709.  
 DEFINITION AR640603 AR640603 AR640603.1 GI:62775412  
 ACCESSION AR640603.1  
 VERSION AR640603.1  
 KEYWORDS Unknown.  
 SOURCE Unclassified.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 508)  
 AUTHORS Conaway,J.W., Conway,R.C. and Kamura,T.  
 TITLE Component of von Hippel-Lindau tumor suppressor complex and SCP  
 ubiquitin ligase  
 JOURNAL Patent: US 6858709-A 3 22-FEB-2005;  
 Oklahoma Medical Research Foundation; Oklahoma City, OK  
 FEATURES Location/Qualifiers  
 SOURCE 1. .508  
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 /mol\_type="genomic DNA"

ORIGIN Alignment Scores:  
 Pred. No.: 2.57e-112 Length: 508  
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 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 6 Gaps: 0

US-09-541-462B-2 (1-108) x AR640603 (1-508)  
 Qy 1 MetAlaAlaAlaMetAspIleValAspIleValAspIleValAspIleValAsp 20  
 Db 7 ATGGCGCAGCGATGGATACCCAGGGCACCAAGGGCAGGGCAGAAG 66  
 Qy 21 ArgPheGluValLysIleSTPAsnAlaValAlaLeuTrpAlaTTPAspIleValAsp 40  
 Db 67 CGCTTGAAGGAAAGTGAATGCGATGCCCTGGCTGGATATGTGGTGTAT 126  
 Qy 41 AsnCysAlaLileCysArgAsnIleMetAspIleValAspIleValAspIleValAsp 20  
 Db 127 AACTGTGCCATTCTGAGAACCATATTGATCTTGCAATAAGCTAACAG 186  
 Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrrGlyValCysAsnHisAlaPheHis 80



RESULT	BC051473	BC051473	mRNA	linear	POD 02-DEC-2004
LOCUS			531 bp	mRNA (cDNA clone MGC:62905 IMAGE:1430400)	
DEFINITION			Mus musculus ring-box 1,		
ACCESSION	BC051473	GI:30186056	complete cds.		
VERSION	MGCG.				
KEYWORDS	Mus musculus (house mouse)				
SOURCE	Mus musculus				
ORGANISM	Mammalia: Butheria; Burchontoglires; Craniata; Vertebrata; Euteleostomi; Eukaryota; Muroidea; Muridae; Murinae; Mus.				
REFERENCE					
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Schuler, G.D., Altschul, S.F., Zeeberg, B.R., Buetow, K.H., Scheuer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.A., Loqueline, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Wooley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzyk, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Fahay, J., Heitton, E., Kettman, M., Maden, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grinwood, J.J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnarch, A., Schein, J.P., Jones, S.J., and Marras, M.A., Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)				
PUBMED	12477932				
REFERENCE	2 (bases 1 to 531)				
AUTHORS	Director MGC Project.				
TITLE	Direct Submission				
JOURNAL	Submitted (28-APR-2003). National Institutes of Health, Mammalian Gene Collection (MGC). Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
NIH-MGC Project URL:	<a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>				
COMMENT	Contact: MGC help desk Email: cgphb-r@mail.nih.gov Tissue Procurement: Marcello Bento Soares, Ph.D. CDNA Library Preparation: M. Bento Soares, University of Iowa DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) <a href="http://www.systemsbiology.org">http://www.systemsbiology.org</a> contact: amaddan@systemsbiology.org				
REMARK	Anup Madan, Jessica Fahay, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting				
LOCATION/QUALIFIERS	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.lnl.nih.gov">http://image.lnl.nih.gov</a> Series: IRAK Plate: 113 Row: e Column: 22 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 40254545.				
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REFERENCE	1 (bases 1 to 535)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Scheuer, C.F., Altschul, S.F., Zeeberg, B.R., Buetow, K.H., Scheuer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Uedin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.A., McEwan, P.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J.,				

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I.I., Skalska, U., Smilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.	Alignment Scores: Pred. No.: 2.69e-112 Score: 108.00 Percent Similarity: 100.0% Best Local Similarity: 100.0% Query Match: 100.0% DB: 8	Length: 535 Matches: 1 Conservative: 0 Mismatched: 0 Indels: 0 Gaps: 0
CONSRM Mammalian Gene Collection Program Team Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences	US-09-541-462B-2 (1-108) × BC001466 (1-535)	
AUTHORS CONSRM Project Direct Submission Submitted (12-DEC-2000) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>	QY Db	QY Db
COMMENT On Sep 16, 2003 this sequence version replaced gi:12655214. Contact: MGC help desk Email: cgapps-request.nih.gov	QY Db	QY Db
REMARK Tissue Preparation: ATCC cDNA Library Arrayed by: The T.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NIISC), Gaithersburg, Maryland, Web site: <a href="http://www.nisc.nih.gov">http://www.nisc.nih.gov</a> Contact: nisc-mgc@nigr.nih.gov	QY Db	QY Db
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Hignight, P., Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R., Maduro, Q.L., Mastello, C., Maskeri, B., Mastriani, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Stranskipop, S., Thomas, P.J., Touchman, J.W., Taurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D.	RESULT 1.9 CR456560 LOCUS CR456560 DEFINITION Homo sapiens RBX1 full length open reading frame (ORF) cDNA clone (CDNA clone C220RF:pcEM.RBX1). ACCESSION CR456560 KEYWORDS CDNA; chromosome 22; ORF. SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo. REFERENCE AUTHORS Edwards, C.A., Davis, M.P., Grinham, J.A., Cole, C.G., Goward, M.B., Aguado, B., Mallya, M., Mokrab, Y., Huckle, E.J., Beare, D.M. and Dunham, J. TITLE Direct Submission JOURNAL Submitted (24-MAY-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: C22g@sanger.ac.uk Manuscript COMMENT Sanger Institute name : pSFM.RBX1 Homo sapiens cDNA sequence. This sequence was generated as part of The Wellcome Trust Sanger Institute program to isolate cDNA clones representing the full length open reading frame of well annotated protein coding genes on human chromosome 22. For more information see <a href="http://www.sanger.ac.uk/HGP/Chr22/">http://www.sanger.ac.uk/HGP/Chr22/</a> . FEATURES source 1..535 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="MGC:1481 IMAGE:3139751" /tissue_type="Placenta, choriocarcinoma" /clone_id="NIH MGC 21" /lab_host="DH10 <sup>R</sup> " /note="vector: pORTB7" gene 1..535 /gene="RBX1" /note="synonyms: ROC1, RNF75, BASS4C12.1, MGC13357," /db_xref="GeneID:9978" /db_xref="MIM:603814" 6..332 /gene="RBX1" /codon_start=1 /product="ring_box 1" /protein_id="AAH01466.1" /db_xref="GI:12655215" /db_xref="GeneID:9978" /db_xref="MIM:603814" /translation="MAAAMDVDPSGTGGAGKRRFEKKWNAVALWAWDIDVNDCAI CRNHFMDLCIECQANQASATSEECTVAVCVMHAFHFCISRLKTRYCPLDNREWE FQKYGH"	Source /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /chromosome="22" Location/Qualifiers 1..535

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**ORIGIN**

Pred. No.:	Alignment Scores:	Length:	Matches:	Conservative:	Percent Similarity:	Best Local Similarity:	Query Match:	DB:
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Db	19 ArgGGGAGCCATGGGTGATAACCCGAGGGCCAACAGGCCGCGGCAAGAAG 78							
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Db	79 CGCTTGTGAAAGTGTGAAAGTGTGATGGCTCTGGCTGGATATTTGTTGTTGAT 138							
Oy	41 AsnCysAlaLeucLysArgAsnHisIleMetAspLeucDysIleGlucysGlnAlaAsnGln 60							
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Oy	101 TrpGluLysGlnLysTrpGlyHis 108							
Db	319 TGGAAATTCCAAAAGATGGCAC 342							

RESULT 20  
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 DEFINITION Homo sapiens (human)  
 KEYWORDS Cds.  
 ORGANISM Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 554)  
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1 (bases 1 to 554)  
 STRAUSBERG, R.L., PEINGOLD, E.A., GROUSE, L.H., DERGE, J.G., KLAUSNER, R.D., COLLINS, F.S., WAGNER, L., SHENMEN, C.M., SCHULER, G.D., ALTSCHUL, S.F., ZEEBERG, B., BUETOW, K.H., SCHAEFER, C.F., BHAT, N.K., HOPKINS, R.F., JORDAN, H., MOORE, T., MAX, S.I., WANG, J., HSIEH, F., DIATCHENKO, L., MARUSINA, K., FARMER, A.A., RUBIN, G.M., HONG, L., SLEPLETON, M., SOARES, M.B., BONALDO, M.J., CASAVANT, T.L., SCHEETZ, T.E., BROWNSTEIN, M.J., USDIN, T.B., TOSHIYUKI, S., CARNINCI, P., PRANGE, C., RAHA, S., LOQUELLANO, N.A., PETERS, G.J.,

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 ORIGIN

Alignment Scores:		Length:		AUTHORS		NIH MGC Project	
Pred.	No.:	2.78e-112	554	Title	CONSUM	Direct Submission	CDNA Library Preparation:
Score:	108.00	Matches:	108	Submitted (25-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA	JOURNAL	Submitted (25-AUG-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Bethesda, MD 20892-2590, USA	NIH MGC Project URL: <a href="http://mgc.ncbi.nlm.nih.gov">http://mgc.ncbi.nlm.nih.gov</a>
Percent Similarity:	100.0%	Conservative:	0	Contact: MGC help desk	COMMENT	Contact: MGC help desk	Email: <a href="mailto:capsbs-r@mail.nih.gov">capsbs-r@mail.nih.gov</a>
Best Local Similarity:	100.0%	Mismatches:	0				
Query Match:	100.0%	Indels:	0				
DB:	8	Gaps:	0				
US-09-541-462B-2 (1-108) × BC017370 (1-554)		Length:		Tissue Procurement:		Dr. Jim Lin, University of Iowa	
Qy	1	MetAlaAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys	20	Procurement:	M. Bento Soares, University of Iowa	Procurement:	CDNA Library Preparation:
Db	23	ATGGCGCAGCGATGGATGGATGAAATGAACTGGCCAAACAGGGGGCAAGAAGAG	82	CDNA Library Arrayed by:	M. Bento Soares, University of Iowa	CDNA Library Arrayed by:	The I.M.A.G.E. Consortium (LNL)
Qy	21	ArgPheGluLysLysIleTPAsnAlaLeuItpAlaItpAspIleValIasp	40	CDNA Sequencing by:	Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada	CDNA Sequencing by:	Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada
Db	83	CGCTTGAGTGAAAGGCAAATGAGTAGGCCCTGGGCTGGAATTGGTTGT	142	Email:	<a href="mailto:info@cgsc.bc.ca">info@cgsc.bc.ca</a>	Email:	<a href="mailto:capsbs-r@mail.nih.gov">capsbs-r@mail.nih.gov</a>
Qy	41	AsnCysSAlaIleCysArgAsnHisIleMetAspIleCysIleGluCysGlnAlaAsn	60	Tissue Procurement:	Dr. Jim Lin, University of Iowa	Tissue Procurement:	CDNA Library Preparation:
Db	143	AACATGTCGATCATGAGAACCCATTAATTGATCTTGATAGATGTCAGCTAACAG	202	Procurement:	M. Bento Soares, University of Iowa	Procurement:	CDNA Library Preparation:
Qy	61	AlaSerAlaThrSerGluLysLysIlePheIleValIlePheIleValIlePheIle	80	CDNA Sequencing by:	Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada	CDNA Sequencing by:	The I.M.A.G.E. Consortium (LNL)
Db	203	GGGTCGCTACTCTGAGAGTGTACTGTCAGAGTCAGCTGCTAACATGCTTTCAC	262	Email:	<a href="mailto:info@cgsc.bc.ca">info@cgsc.bc.ca</a>	Email:	<a href="mailto:capsbs-r@mail.nih.gov">capsbs-r@mail.nih.gov</a>
Qy	81	PheHisCysIleSerArgTrpLeuIleSerArgTrpIleValIlePheIleValIlePheIle	100	Tissue Procurement:	Dr. Jim Lin, University of Iowa	Tissue Procurement:	CDNA Library Preparation:
Db	263	TTCCACTGATCATCTCGCTGCTCAAAACAGACAGGGTGTCCATGGACAACAGAG	322	Procurement:	M. Bento Soares, University of Iowa	Procurement:	CDNA Library Preparation:
Qy	101	TrpGluIpheIleValIlePheIleValIlePheIleValIlePheIleValIlePheIle	108	CDNA Sequencing by:	Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada	CDNA Sequencing by:	The I.M.A.G.E. Consortium (LNL)
Db	323	TGGGAATTCAAAAGTATGGCAC	346	Email:	<a href="mailto:info@cgsc.bc.ca">info@cgsc.bc.ca</a>	Email:	<a href="mailto:capsbs-r@mail.nih.gov">capsbs-r@mail.nih.gov</a>
RESULT 21		BC056992		Length:		Organism:	
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DEFINITION							
ACCESSION		BC056992		clone	MG:66938 IMAGE:6818827"		
VERSION		BC056992..1					
KEYWORDS							
SOURCE							
ORGANISM							
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1 (bases 1 to 1612)							
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Schuler, G.D.,							
Altshuler, R.D., Collins, F.S., Wagner, L., Shemesh, C.M., Schaefer, C.F., Bhat, N.K.,							
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Carninci, P., Prange, C., Raha, S., Loqueline, N.S., Peters, G.J., Abramson, R.D., Mullally, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,							
Worley, K.C., Hale, S., Garcia, A.M., Gey, L.J., Hulyk, S.W., Villalon, D.K., Murzy, D.M., Soderoren, E.J., Liu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettenen, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalius, D.B., Schnurch, A., Schein, J.E., Jones, S.J. and Marra, M.A.							
Mammalian Gene Collection Program Team							
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences							
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)							
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TITLE							
JOURNAL							
PUBMED							
REFERENCE							
AUTHORS							
Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Schuler, G.D.,							
Altshuler, R.D., Collins, F.S., Wagner, L., Shemesh, C.M., Schaefer, C.F., Bhat, N.K.,							
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Worley, K.C., Hale, S., Garcia, A.M., Gey, L.J., Hulyk, S.W., Villalon, D.K., Murzy, D.M., Soderoren, E.J., Liu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettenen, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalius, D.B., Schnurch, A., Schein, J.E., Jones, S.J. and Marra, M.A.							
Mammalian Gene Collection Program Team							
Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences							
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)							
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 complete cds.

ACCESSION BC027396  
 VERSION 1 GI:20072075  
 MGC.  
 SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciuromorpha; Muridae; Murinae; Mus.  
 1 (bases 1 to 1616)

Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,  
 Collins FS, Wagner L, Shamen CM, Schulz GD, Altenschul SF, Zeeberg  
 B, Buetow KH, Schaefer CF, Bhattacharjee A, Jordan H, Moore T,  
 Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin  
 GM, Hong L, Stapleton M, Soares MB, Borodl MF, Casavant TL,  
 Scheetz TE, Brownstein MJ, Uedin TB, Toshiyuki S, Carrinci P,  
 Prange C, Raha SS, Loqueland NA, Peters GA, Abramson RD, Mullahy  
 SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH,  
 Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW,  
 Villalon DK, Muzny DM, Soderren EJ, Lu X, Gibbs RA, Fahey J,  
 Helton E, Kettman M, Madan A, Rodrigues S, Sanchez A, Whiting M,  
 Madan A, Young AC, Bouffard GG, Blakesley RW,  
 Touchman JW, Green BD, Dickson MC, Rodriguez AC, Grinwood J,  
 Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,  
 Smialski DE, Schnerch A, Schein JE, Jones SJ and Marra MA.

REFERENCE Mammalian Gene Collection Program Team  
 Generation and initial analysis of more than 15,000 full-length  
 human and mouse cDNA sequences  
 Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

JOURNAL J. Clin. Microbiol. 41(12):6292-6297 (2003)  
 PUBMED 1479932  
 AUTHORS Director MGC Project  
 TITLE Submitted (04-APR-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA  
 NIH-MGC Project URL: http://mgc.nci.nih.gov  
 COMMENT Contact: MGC help desk  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Jeffrey Green M.D.  
 DNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Baylor College of Medicine Human Genome  
 Sequencing Center  
 Center code: BCM-HGSC  
 Web site: http://www.hgsc.bcm.edu/cdna/  
 Contact: amg@bcm.edu  
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Louiseed, H.,  
 Kovis, C.R., Sneed, A.J., Martin, R.G., Muzny, D.M., Nanavati,  
 A.N., Gibbs, R.A.

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 Db 247 TTCCACTGCACTCTGATGGTACGTTGATGGACTGGAGCTGGAGAG 306  
 Qy 101 TrpGluPheGlnLysTerGlyHis 108  
 Db 307 TGGAGTTCCGAAGTATGGCAT 330

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Run on: March 11, 2006, 08:44:10 ; Search time 166 Seconds  
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SUMMARIES

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2	10.8	100.0	504	3	US-09-914-324A-5		Sequence 5, Appli
3	10.8	100.0	507	3	US-09-949-016-4940		Sequence 4940, Ap
4	10.8	100.0	508	3	US-09-914-324A-3		Sequence 3, Appli
5	8.4	77.8	3208	3	US-09-780-016-27		Sequence 27, Appli
6	8.4	77.8	3208	3	US-10-214-811-27		Sequence 27, Appli
7	8.4	77.8	3208	3	US-10-766-074-27		Sequence 27, Appli
8	7.4	68.5	411	3	US-09-640-211-1731		Sequence 1731, Ap
9	5.5	50.9	402	3	US-09-513-999C-10371		Sequence 10371

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
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2	10.8	100.0	504	3	US-09-914-324A-5		Sequence 5, Appli
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5	8.4	77.8	3208	3	US-09-780-016-27		Sequence 27, Appli
6	8.4	77.8	3208	3	US-10-214-811-27		Sequence 27, Appli
7	8.4	77.8	3208	3	US-10-766-074-27		Sequence 27, Appli
8	7.4	68.5	411	3	US-09-640-211-1731		Sequence 1731, Ap
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SUMMARIES

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ALIGNMENTS

RESULT 1  
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   Sequence 3894, Application US/09513999C  
   Patent No. 6783961  
   GENERAL INFORMATION:  
     APPLICANT: Dumas Milne Edwards, J. B.  
     APPLICANT: Ducimet, A.  
     APPLICANT: Giordano, J. Y.  
   TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
   Patent No. 6783961  
   FILE REFERENCE: 59 US2 REG  
   CURRENT APPLICATION NUMBER: US/09/513,999C  
   CURRENT FILING DATE: 2000-02-24  
   PRIOR APPLICATION NUMBER: US 60/122,487  
   PRIOR FILING DATE: 1999-12-26  
   NUMBER OF SEQ ID NOS: 36681  
   SOFTWARE: Patent.pm  
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   ORGANISM: Homo sapiens  
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     NAME/KEY: CDS  
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QY 101 TrpGluPheGlnLysTrgLyHis 108  
 DB 329 TGGGAATTCCAAAAGTATGGCAC 352

**RESULT 2**

US-09-914-324A-5  
 Sequence 5, Application US/09914324A

GENERAL INFORMATION:  
 Patent No. 6858709  
 APPLICANT: Conway, Joan A.  
 APPLICANT: Conway, Ronald C.  
 APPLICANT: Kamura, Takumi  
 APPLICANT: Oklahoma Medical Research Foundation  
 TITLE OF INVENTION: No. 6858709e1 Component of von Hippel-Lindau Tumor Suppressor  
 CURRENT APPLICATION NUMBER: WO/PCT/US00/04838  
 FILE REFERENCE: 021044-004600US  
 CURRENT FILING DATE: 2000-02-25  
 PRIORITY NUMBER: US 60/121,787  
 PRIOR FILING DATE: 1999-02-26  
 PRIOR APPLICATION NUMBER: WO/PCT/US00/04838  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: PatentIn Ver. 2.1  
 SEQ ID NO 5  
 LENGTH: 504  
 TYPE: DNA  
 ORGANISM: Mus sp.  
 FEATURE: CDS  
 NAME/KEY: CDS  
 LOCATION: (18)..(344)  
 OTHER INFORMATION: Rbx1  
 US-09-914-324A-5

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QY 21 AsnCysAlaIleCysArgAsnHiSileLeuAspIeuCysCysInAlaAsnGln 60  
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QY 61 AlaSerAlaThrSerGluGluCysTrpGlyValCysAsnHiAlaPheHi 80  
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QY 81 PheHiCysIleSerArgTrpLeuLysTrpArgInvalCysProLeuAspAsnArgGlu 100  
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QY 101 TrpGluPheGlnLysTrgLyHis 108  
 Db 307 TGGGAATTCCAAAAGTATGGCAC 330

RESULT 4  
 US-09-914-324A-3  
 Sequence 3, Application US/09914324A  
 GENERAL INFORMATION:  
 Patent No. 6858709  
 APPLICANT: Conway, Joan A.  
 APPLICANT: Conway, Ronald C.  
 APPLICANT: Kamura, Takumi  
 TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase  
 FILE REFERENCE: 021044-004600US  
 CURRENT FILING DATE: 2003-02-11  
 PRIORITY NUMBER: US 60/121,787  
 PRIOR FILING DATE: 1999-02-26  
 PRIORITY NUMBER: WO/PCT/US00/04838  
 PRIOR FILING DATE: 2000-02-25  
 PRIORITY NUMBER: 6812339

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 US-09-949-016-4940  
 Sequence 4940, Application US/09949016  
 Patent No. 6812339

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; NAME/KEY: CDS
; LOCATION: (7)..(333)
; OTHER INFORMATION: Rxr1
US-09-914-324A-3

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Qy 85 SerArgTrpLeuIlysThrArgGlnValCysProLeuAspAsnArgGluTrpGlupheGln 104
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Qy 105 LysTrpGlyHiS 108
Db 3010 AAAGTAGGGCAC 3021

RESULT 6
US-10-214-811-27
; Sequence 27, Application US/10214811
; Patent No. 6745621
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/10/214, 811
; CURRENT FILING DATE: 2002-08-07
; PRIORITY NUMBER: US/09/780, 016
; PRIOR FILING DATE: 2001-02-09
; PRIORITY NUMBER: US 60/181, 294
; PRIORITY NUMBER: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
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; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-214-811-27

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DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-214-811-27 (1-3208)

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Qy 45 CysArgAsnHisIleMetAspLencySleGluCysGlnAlaAsnGlnAlaSerAlaThr 64
Db 2830 TGCAAGAACACATTAGCATTCATGAACTTGCATAAGATCAGCTAAACAGGCTCCGCTACT 2889

Qy 65 SerGluGluCysThrValAlaTrpGlyValCysAsnHiSalpheHiPheHiCysSle 84
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Qy 85 SerArgTrpLeuIlysThrArgGlnValCysProLeuAspAsnArgGluTrpGlupheGln 104
Db 2950 TCTCGCTGGCTCAAACACGACAGTTGACAGTGAACTGGATTCCA 3009

Qy 105 LysTrpGlyHiS 108
Db 3010 AAAGTAGGGCAC 3021

RESULT 5
US-09-780-016-27
; Sequence 27, Application US/09780016
; Patent No. 6509456
; GENERAL INFORMATION:
; APPLICANT: Donoho, Gregory
; APPLICANT: Scoville, John
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Friedrich, Glenn
; APPLICANT: Abuin, Alejandro
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur T.
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0132-USA
; CURRENT APPLICATION NUMBER: US/09/780, 016
; CURRENT FILING DATE: 2001-02-09
; PRIORITY NUMBER: US 60/181, 294
; PRIORITY NUMBER: 2000-02-11
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 27
; LENGTH: 3208
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-214-811-27

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Pred. No.: 1.71e-82 Length: 3208
Score: 84.00 Matches: 84
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 77.8% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-214-811-27 (1-3208)

Qy 25 LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsnCysAlaIle 44
Db 2770 AAAATAATGGAAATGAGGTGCCCTGGCTGGATATCTGTGCATC 2829

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QY 45 CysArgAsnHisIleMetAspLeuCysIleGluCysGlnLalaAsnGlnAlaSerAlaThr 64  
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QY 65 SerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaLpheHiSphcHisCysIle 84  
QY 2890 TCAAGAGGTGACTGTGATGGGAGTCGTAACCGTTAACACTGCACTGCACT 2949

QY 85 SerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGln 104  
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QY 105 LysTyrGlyHis 108  
QY 3010 AAGTATGGGCAC 3021

RESULT 7  
; Sequence 27, Application US/10766074  
; Patent No. 6881563  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Scoville, John  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Abuin, Alejandro  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: No. 6881563 e1 Human Proteases and  
; TITLE OF INVENTION: Polynucleotides Encoding the Same  
; FILE REFERENCE: LEX-0132-USA  
; CURRENT APPLICATION NUMBER: US/10/7665, 074  
; CURRENT FILING DATE: 2004-01-28  
; PRIOR APPLICATION NUMBER: US/10/214, 811  
; PRIOR FILING DATE: 2002-08-07  
; PRIOR APPLICATION NUMBER: US/09/780, 016  
; PRIOR FILING DATE: 2001-02-09  
; PRIOR APPLICATION NUMBER: US 60/181, 294  
; PRIOR FILING DATE: 2000-02-11  
; NUMBER OF SEQ ID NOS: 27  
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; TYPE: DNA  
; ORGANISM: homo sapiens  
; US-10-766-074-27

RESULT 8  
; Sequence 1731, Application US/09640211A  
; Patent No. 6833446  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; APPLICANT: Shenk, Michael A.  
; APPLICANT: McGrath, Annette  
; APPLICANT: Glenn, Matthew  
; TITLE OF INVENTION: Compositions and Methods for the  
; Modification of Gene Transcription  
; FILE REFERENCE: 110000.1021CU  
; CURRENT APPLICATION NUMBER: US/09/640, 211A  
; CURRENT FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 2368  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 1731  
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; TYPE: DNA  
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; FEATURE: misc feature  
; NAME/KEY: misc feature  
; LOCATION: (1) .(411)  
; OTHER INFORMATION: n = A,T,C or G  
; US-09-64-211A-1731

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Query Match: 68.5% Indels: 0  
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-640-211A-1731 (1-411)

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QY 45 CysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThr 64  
QY 236 TGCGAAACACATCATGACCCTCTGTATTGACTGTAGCTGAGCAAAATCAAGCAAGTCAACA 2999

QY 65 SerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaLpheHiSheHiCysIle 84  
QY 296 AGTGAAGATGACTGTGATGGCATGGTGTGAAATCAGGCCCTTCATTCCATTGCATA 3552

QY 85 SerArgTrpLeuLysThrArgGlnValCysProLeuAspAsn 98  
QY 356 AGTGGTGGCTAAAGCACGACAGTCGCCATTAGATAAT 397

RESULT 9  
; Sequence 10371, Application US/09513999C  
; Patent No. 6793961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.-B.  
; APPLICANT: Dufclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513, 999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122, 487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent .pm

QY 25 LysLysTrpAsnAlaLeuTrpAlaTrpAspIleValAspAsnCysAlaIle 44  
QY 2770 AAAAATGGAATGGCAGTAGGCCCTGGATATGCTGAAACTGTGCACT 2829

QY 45 CysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThr 64  
QY 2830 TCGAGGAACCATTTGATCTTGCATAGAATGTCAGCTAACAGGGTCCGCTACT 2889

QY 65 SerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaLpheHiSphcHisCysIle 84  
QY 2890 TCAAGAGGTGACTGTGCTGCGATGGGAGTCGAACCTTCACTTCAGTC 2949

QY 85 SerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGln 104  
QY 2950 TCTCGCTGGCTCAAACAGGAGCTGGATTCAGGATTCAGGAAATTCCA 3009

```

: SEQ ID NO 10371
: LENGTH: 402
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 20
: OTHER INFORMATION: k=g or t
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 38
: OTHER INFORMATION: s=g or c
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 79
: OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-10371

Alignment Scores:
Pred. No.: 1.76e-51 Length: 402
Score: 55.00 Matches: 55
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 50.9% Indexes: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-513-999C-10371 (1-402)
Qy 54 IleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGly 73
Db 108 ATAGAATGTCAGCTAACCGTGTACTTCAGAAGAGGTGACTGTGGCATGGGA 167

RESULT 10
Qy 74 ValCysAsnHisAlaPheHisCysIleSerArgTrpLeuLysThrArgGlnVal 93
Db 168 GTCTGPAACCATGCTTTCACCTCCACTGCAAAACGAGCAGGTG 227

Qy 94 CysProIleAspAsnArgGluTrpGluPheGlnLysTrpGlyHis 108
Db 228 TGTCATTGGACAACAGAGTGGAATTCCAAGATGGCAC 272

RESULT 10
US-09-621-976-15180
: Sequence 15180, Application US/09621976
: Patent No. 6539063
: GENERAL INFORMATION:
:   APPLICANT: Dumas Milne Edwards, J.B.
:   APPLICANT: Jobert, S.
:   APPLICANT: Giordano, J.Y.
:   TITLE OF INVENTION: ESTs and Encoded Human Proteins.
:   FILE REFERENCE: GENSET_054R2
:   CURRENT APPLICATION NUMBER: US/09/621,976
:   CURRENT FILING DATE: 2000-07-21
:   NUMBER OF SEQ ID NOS: 19335
:   SOFTWARE: Patent_pm
:   SEQ ID NO 15180
:   LENGTH: 463
:   TYPE: DNA
:   ORGANISM: Homo sapiens
:   FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: 74
:   OTHER INFORMATION: n=a, g, c or t
US-09-621-976-15180

Alignment Scores:
Pred. No.: 2e-51 Length: 463
Score: 55.00 Matches: 55
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 50.9% Indexes: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-621-976-15180 (1-463)

Qy 54 IleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGly 73
Db 103 ATAGAATGTCAGCTAACCGTGTACTTCAGAAGAGGTGACTGTGGCATGGGA 162

Qy 74 ValCysAsnHisAlaPheHisCysIleSerArgTrpLeuLysThrArgGlnVal 93
Db 163 GTCTGPAACCATGCTTTCACCTCCACTGCAAAACGAGCAGGTG 222

Qy 94 CysProIleAspAsnArgGluTrpGluPheGlnLysTrpGlyHis 108
Db 223 TGTCATTGGACAACAGAGTGGAATTCCAAGATGGCAC 267

RESULT 11
US-09-313-294A-492
: Sequence 492, Application US/09313294A
: Patent No. 6476212
: GENERAL INFORMATION:
:   APPLICANT: Laligudi, Raghunath V.
:   APPLICANT: Ito, Lura Y.
:   APPLICANT: Sherman, Bradley K.
:   TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US
:   CURRENT APPLICATION NUMBER: US/09/313,294A
:   CURRENT FILING DATE: 1999-05-14
:   NUMBER OF SEQ ID NOS: 7600
:   SOFTWARE: PBRl Program
SEQ ID NO 492
Length: 301
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 7005493335H1
US-09-313-294A-492

Alignment Scores:
Pred. No.: 3.95e-35 Length: 301
Score: 40.00 Matches: 40
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 37.0% Indexes: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-313-294A-492 (1-301)
Qy 25 LysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAlaAspLysCysAlaIle 44
Db 181 AAGAAGTGGAAACGGGTCTGGCATGGATATCTGGTGCACACTGGCTATC 240

Qy 45 CysArgAsnHisIleMetAspLeuCysIleGlucySGlnAlaAsnGlnAlaSerAlaThr 64
Db 241 TGCGGCAACCACATCATGGATCTATGCAATGAGGCCAGGGGAC 300

RESULT 12
US-09-949-016-16682
: Sequence 16682, Application US/09949016
: Patent No. 6812319
: GENERAL INFORMATION:
:   APPLICANT: Venter, J. Craig et al.
:   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
:   CURRENT APPLICATION NUMBER: US/09/949,016
:   CURRENT FILING DATE: 2000-04-14
:   PRIORITY APPLICATION NUMBER: 60/241,755
:   PRIORITY FILING DATE: 2000-10-20
:   PRIORITY APPLICATION NUMBER: 60/237,768
:   PRIORITY FILING DATE: 2000-10-03
:   PRIORITY APPLICATION NUMBER: 60/231,498
:   PRIORITY FILING DATE: 2000-09-08
:   NUMBER OF SEQ ID NOS: 207012
:   SOFTWARE: FastSeq For Windows Version 4.0

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```

; SEQ ID NO 16682
; LENGTH: 25274
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16682

Alignment Scores:
Pred. No : 2.666-21 Length: 25274
Score: 29.00 Matches: 29
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 26.9% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-949-016-16682 (1-25274)
QY    77 HisAlaPheHisCysIleSerArgTPLEuLysThrArgGlnValCysProLeu 96
Db     18411 CATGCTTTCACTTCACATTCACATCCTCGTGGCTCAAAACAGAACAG 18470

QY    97 AspAsnArgGluLrpGluPheGlnIys 105
Db     18471 GACAACGAGATGGGAATTCCAAAAG 18497

RESULT 13
US-09-914-324A-4
Sequence 4, Application US/09914324A
GENERAL INFORMATION:
; Patent No. 6858709
; APPLICANT: Conaway, Joan A.
; APPLICANT: Conaway, Ronald C.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklahoma Medical Research Foundation von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: No. 6858709 Del Component of von Hippel-Lindau Tumor Suppressor
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; FILE REFERENCE: 021044-004600US
; CURRENT APPLICATION NUMBER: US09/914,324A
; CURRENT FILING DATE: 2003-02-11
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: WO PCT/US00/04838
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 480
TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: (4)..(369)
OTHER INFORMATION: Rbx1
US-09-914-324A-4

Alignment Scores:
Pred. No.: 0.00033 Length: 480
Score: 12.00 Matches: 12
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 11.1% Indels: 0
DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-949-324A-4 (1-480)
QY    39 ValAspAsnCysAlaIleCysArgAsnHistileMet 50
Db     157 GTTGACAACTGTGCATTGCGAACATAATG 192

RESULT 14
US-09-270-767-26812/c
; Sequence 26812, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 11, 2006, 09:45:04 ; Search time 653 Seconds

(without alignments)

1367.677 Million cell updates/sec

Title: US-09-541-462B-2

Perfect score: 108

Sequence: 1 MAAMDVDTPSGTNSGAGKK.....KTRQVCPLDNREWEFQKYGH 108

Scoring table: OLIGO

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Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 9793542 seqs, 4134689005 residues

Word size: 12

Total number of hits satisfying chosen parameters: 119

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-DB=Published\_Applications\_NA\_Main -QFMFT=fastap -SUFFIX=o190.rnbp  
-MINMATCH=0.1 -LOOPC1=0 -LOOPC2=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo  
-TRANS=human40\_cdi -LIST=0 -DCALIGN=200 -THR SCORE=quality -THR MIN=12  
-ALIGN=15 -MODEB=LOCAL -OUTFMT=o1o -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=2000000000 -HOST=abs100h  
-NO\_KMAP -NBG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120  
-WARN TIMEOUT=30 -TREADS=1 -XGAPPOP=60 -XGAPEXT=60 -FGAPPOP=6 -FGAPEXT=7  
-YGAPOP=60 -YGAPEXT=60 -DELEXT=6 -DEL0P=6 -DELEXT=7

Database : Published\_Applications\_NA\_Main:\*

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2: /cgn2\_6/pctodata/1/pubpna/US08\_PUBCOMB.seq:\*

3: /cgn2\_6/pctodata/1/pubpna/US09A\_PUBCOMB.seq:\*

4: /cgn2\_6/pctodata/1/pubpna/US09B\_PUBCOMB.seq:\*

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6: /cgn2\_6/pctodata/1/pubpna/US10B\_PUBCOMB.seq:\*

7: /cgn2\_6/pctodata/1/pubpna/US10C\_PUBCOMB.seq:\*

8: /cgn2\_6/pctodata/1/pubpna/US10D\_PUBCOMB.seq:\*

9: /cgn2\_6/pctodata/1/pubpna/US10E\_PUBCOMB.seq:\*

10: /cgn2\_6/pctodata/1/pubpna/US11\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	108	100.0	433	7 US-10-242-535A-43377	Sequence 43377, A
2	108	100.0	433	7 US-10-085-783A-56068	Sequence 56068, A
3	108	100.0	453	7 US-10-242-535A-56068	Sequence 56068, A
4	108	100.0	453	7 US-10-085-783A-46292	Sequence 46292, A
5	108	100.0	467	7 US-10-242-535A-46292	Sequence 46292, A
6	108	100.0	467	7 US-10-085-783A-46292	Sequence 46292, A
7	108	100.0	471	7 US-10-242-535A-57254	Sequence 57254, A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### ALIGNMENTS

RESULT 1	/ Sequence 43377, Application US/10242535A
	; GENERAL INFORMATION:
	; PUBLICATION NO. US20040103663A1
	; APPLICANT: ChondroGene Inc.
	; APPLICANT: Lieuw, C.C.
	; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
	; FILE REFERENCE: 4231/2005
	; CURRENT APPLICATION NUMBER: US/10-242-535A
	; FILING DATE: 2002-09-12
	; PRIOR APPLICATION NUMBER: US 10-085,783
	; PRIOR FILING DATE: 2002-02-28
	; PRIOR APPLICATION NUMBER: US 60/305,340
	; PRIOR FILING DATE: 2001-07-13
	; NUMBER OF SEQ ID NOS: 58994
	; SOFTWARE: PatentIn version 3.2
	; SEQ ID NO: 43377
	; LENGTH: 433
	; TYPE: DNA
	; ORGANISM: Human
	; Alignment Scores:
	; Pred. No.: 9,41e-111
	; Score: 108.00
	; Percent Similarity: 100.0%



Qy 101 TrpGlpheGlnIysTrgLyHis 108  
 Db 324 TGGAAATTCCAAAAGTATGGCAC 347

RESULT 4  
 US-10-085-783A-35025  
 ; Sequence 35025, Application US/10085783A  
 ; Publication No. US20040037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; ATTORNEY: Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US/10/085 , 783A  
 ; PRIOR APPLICATION NUMBER: US 60/305,340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: US 60/275,017  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIOR APPLICATION NUMBER: US 60/271,955  
 ; PRIOR FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 39933  
 ; LENGTH: 467  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-10-242-535A-39933

Alignment Scores:  
 Pred. No.: 1.00e-110 Length: 467  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-39933 (1-467)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20  
 Db 20 ATGGCGGAGGCTATGGATGTGATAACCCGAGGGACCAAGGCCGCGCAGAG 79

Alignment Scores:  
 Pred. No.: 1.00e-110 Length: 467  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-35025 (1-453)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20  
 Db 20 GGTGCCCCTACTCAGAGGTACTGTCGATGGGAGGTTGTACCATGCTTCAC 25

Alignment Scores:  
 Pred. No.: 9.79e-111 Length: 453  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-35025 (1-453)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20  
 Db 20 GGTGCCCCTACTCAGAGGTACTGTCGATGGGAGGTTGTACCATGCTTCAC 25

Alignment Scores:  
 Pred. No.: 9.79e-111 Length: 453  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

Qy 21 ArgPheGluValAlaLysTrpAsnAlaValAlaLeuTrpAspIleValValAsp 40  
 Db 20 CGCTTGAGTGTAAAAGTGAATCTGGATATCTGGTGAT 143

Alignment Scores:  
 Pred. No.: 108.00 Length: 453  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

Qy 21 ArgPheGluValAlaLysTrpAsnAlaValAlaLeuTrpAspIleValValAsp 40  
 Db 20 CGCTTGAGTGTAAAAGTGAATCTGGATATCTGGTGAT 143

Qy 61 AlaSerAlaLysTrpAsnAlaValAlaLeuTrpAspIleValValAsp 40  
 Db 20 GGTGCCCCTACTCAGAGGTACTGTCGATGGGAGGTTGTACCATGCTTCAC 25

Alignment Scores:  
 Pred. No.: 108.00 Length: 453  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

Qy 61 AlaSerAlaLysTrpAsnAlaValAlaLeuTrpAspIleValValAsp 40  
 Db 20 GGTGCCCCTACTCAGAGGTACTGTCGATGGGAGGTTGTACCATGCTTCAC 25

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 260 TCTCACATGCACTCTCTGGCTCAAACACCAAGGTGTGTCATGGACACAGAGAG 311

Alignment Scores:  
 Pred. No.: 108.00 Length: 453  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 260 TCTCACATGCACTCTGGCTCAAACACCAAGGTGTGTCATGGACACAGAGAG 311

Qy 101 TrpGluIleGlnLysIleYTGlyHis 108  
 Db 320 TGGAAATTCCAAAAGTATGGGCAC 343

RESULT 6  
 US-10-085-783A-39933  
 ; Sequence 39933, Application US/10085783A  
 ; Publication No. US20040037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; ATTORNEY: Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US/10/085,783A  
 ; CURRENT FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/305,340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: US 60/275,017  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIOR APPLICATION NUMBER: US 60/271,955  
 ; PRIOR FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 39933  
 ; LENGTH: 467  
 ; TYPE: DNA

RESULT 5  
 US-10-242-535A-39933  
 ; Sequence 39933, Application US/1024253A1  
 ; Publication No. US20040013663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; ATTORNEY: Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2005  
 ; CURRENT APPLICATION NUMBER: US/10/242-535A  
 ; CURRENT FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/305,340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: US 60/275,017  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIOR APPLICATION NUMBER: US 60/271,955  
 ; PRIOR FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 39933  
 ; LENGTH: 467  
 ; TYPE: DNA

ORGANISM: Human  
US-10-085-783A-3933

Alignment Scores:  
Pred. No.: 1.01e-110 Length: 467  
Score: 108.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Minimatches: 0  
Query Match: 100.0% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) × US-10-085-783A-39933 (1-467)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysIys 80  
Db 20 ATGGCGGAGGGATGGATGTGGATACTGGATTCACGGGGCAAGGAG 79

Qy 21 ArgPheGluvalLysStpAsnAlaValAlaLeutRpAlaTrpAspIleValValAsp 40  
Db 77 CGTTTGAAGTGAAAGTGGATGCAGTAGCCCTCTGGCTGGATATTGGTTGAT 136

Qy 41 AsnCysAlaIleCysArgAsnIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60  
Db 137 AACTGTGCATCTGAGAAACCATAATGGATCTTGATGATGAACTGAACTCAG 196

Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaItrpGlyValCysAsnHisAlaPheHis 80  
Db 197 GCnCCGCTACTTCAGAGAGTGACTGCGATGGAGTGCTGAACTATGTTTAC 256

Qy 81 PheHisCysIleSerArgTpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
Db 257 TTCCACTGCTATCTCGCTGCCAAACAGCACAGGTGTCATTGACAAAGAGAG 316

Qy 101 TrpGluPheGlnLysStryGlyHis 108  
Db 317 TGGGAATCCAAAGATGGGCAC 340

RESULT 8  
US-10-085-783A-57254  
; Sequence 57254, Application US/10085-783A  
; Publication No. US20040037841A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; ATTORNEY OR AGENT: Liew, C. C.  
; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis  
; FILE REFERENCE: 4231/2002  
; CURRENT APPLICATION NUMBER: US 60/305,340  
; PRIOR APPLICATION NUMBER: US 60/07-13  
; PRIOR FILING DATE: 2001-07-13  
; FILE REFERENCE: 4231/2002  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; SEQ ID NO: 57254  
; LENGTH: 471  
; TYPE: DNA  
; ORGANISM: Human  
US-10-085-783A-57254  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
Alignment Scores:  
Pred. No.: 1.00e-110 Length: 471  
Score: 108.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Minimatches: 0  
Query Match: 100.0% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) × US-10-085-783A-57254 (1-471)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyAlaGlyLysIys 20  
Db 17 ATGGCGGAGGGATGGATGTGGATACTGGATTCACGGGGCAAGGAG 76

Qy 21 ArgPheGluvalLysStpAsnAlaValAlaLeutRpAlaTrpAspIleValValAsp 40  
Db 77 CGTTTGAAGTGAAAGTGGATGCAGTAGCCCTCTGGCTGGATATTGGTTGAT 136

Qy 41 AsnCysAlaIleCysArgAsnIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60  
Db 137 AACTRGCGCATCTGGAGAACAACTTGGATCTGGATAGAACTGCAAGTAACTCAG 196

Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaItrpGlyValCysAsnHisAlaPheHis 80

RESULT 9  
US-10-085-783A-57254  
; Sequence 57254, Application US/10085-783A  
; Publication No. US20040037841A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; ATTORNEY OR AGENT: Liew, C. C.  
; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis  
; FILE REFERENCE: 4231/2002  
; CURRENT APPLICATION NUMBER: US 60/305,340  
; PRIOR APPLICATION NUMBER: US 60/07-13  
; PRIOR FILING DATE: 2001-07-13  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; PRIOR APPLICATION NUMBER: US2004013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; ATTORNEY OR AGENT: Liew, C. C.  
; TITLE OF INVENTION: Compositions and Methods Relatiing to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; PRIOR APPLICATION NUMBER: US 60/07-13  
; PRIOR FILING DATE: 2001-07-12  
; PRIOR APPLICATION NUMBER: US 60/085,783  
; PRIOR FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 57254  
; LENGTH: 471  
; TYPE: DNA  
; ORGANISM: Human  
US-10-085-783A-57254  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 57254  
; LENGTH: 471  
; TYPE: DNA  
; ORGANISM: Human  
US-10-242-535A-57254  
Alignment Scores:  
Pred. No.: 1.00e-110 Length: 471  
Score: 108.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Minimatches: 0  
Query Match: 100.0% Indels: 0  
DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) × US-10-085-783A-57254 (1-471)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyAlaGlyLysIys 20  
Db 17 ATGGCGGAGGGATGGATGTGGATACTGGATTCACGGGGCAAGGAG 76

Qy 21 ArgPheGluvalLysStpAsnAlaValAlaLeutRpAlaTrpAspIleValValAsp 40  
Db 77 CGTTTGAAGTGAAAGTGGATGCAGTAGCCCTCTGGCTGGATATTGGTTGAT 136

Qy 41 AsnCysAlaIleCysArgAsnIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60  
Db 137 AACTRGCGCATCTGGAGAACAACTTGGATCTGGATAGAACTGCAAGTAACTCAG 196

Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaItrpGlyValCysAsnHisAlaPheHis 80



RESULT 11  
US-10-913-937-5  
Sequence 5, Application US/10913937  
Publication No. US20050019813A1  
GENERAL INFORMATION:  
APPLICANT: Conaway, Joan A.  
APPLICANT: Conaway, Ronald C.  
APPLICANT: Kamura, Takumi  
APPLICANT: Oklamona Medical Research Foundation  
TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor  
TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor  
FILE REFERENCE: 021044-004600US  
CURRENT APPLICATION NUMBER: US/10/913,937  
CURRENT FILING DATE: 2004-08-05  
PRIOR APPLICATION NUMBER: US/09/914,324  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: US 60/121,787  
TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor  
TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase  
FILE REFERENCE: 021044-004600US  
CURRENT APPLICATION NUMBER: US/10/913,937  
CURRENT FILING DATE: 2004-08-05  
PRIOR APPLICATION NUMBER: US/09/914,324  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: WO PCT/US00/04838  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 5  
LENGTH: 504  
TYPE: DNA  
ORGANISM: Mus sp.  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (18)..(344)  
OTHER INFORMATION: Rbx1  
US-10-913-937-5

Alignment Scores:  
Pred. No.: 1.08e-110 Length: 504  
Score: 108.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 8 Gaps: 0  
DB: US-10-913-937-5 (1-504)

US-09-541-462B-2 (1-108) × US-10-913-937-3 (1-508)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20  
Db 18 ATGGCCGGGGATGTGGATACCCAGGCCACAGGGCAGGGATCTGGATACGGCAACAGGGCAGGGAG 77  
Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeutTpAlaTrpAspIleValValAsp 40  
Db 78 CGCTTGAAAGTTAAAAGTGAATGAACTGGATGTCATGGACATTGTGCTTGAT 137  
Qy 41 AsnCysAlaLysCysArgAsnHisIleMetAspLeuCysTrpGlyAlaGlyLys 20  
Db 138 AACGTGCCATTCGAGAACACATTATGATCTTGTACGATCTGGCAACACAG 197  
Qy 61 AlaSerAlaThrSerGluCysTrpGlyValCysAsnHisAlaPheHis 80  
Db 198 GCGTCAGCTACTCCAAAGACTGTAGATGGCAACAGTGCTCAAACAGAGAG 306  
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
Db 258 TTCCACTGCACTCTCGATGGCTCAAACGGGCACTGGTGTGCTGGCAACAGAGAG 317  
Qy 101 TrpGluPheGlnLysLysTyrGlyHis 108  
Db 318 TGGAGTTCCAAGATGGCAT 341

RESULT 12  
US-10-913-937-3  
Sequence 3, Application US/10913937  
Publication No. US20050019813A1  
GENERAL INFORMATION:  
APPLICANT: Conaway, Joan A.

APPLICANT: Conaway, Ronald C.  
APPLICANT: Kamura, Takumi  
APPLICANT: Oklamona Medical Research Foundation  
TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor  
TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor  
FILE REFERENCE: 021044-004600US  
CURRENT APPLICATION NUMBER: US/10/913,937  
CURRENT FILING DATE: 2004-08-05  
PRIOR APPLICATION NUMBER: US/09/914,324  
PRIOR FILING DATE: 2001-08-22  
PRIOR APPLICATION NUMBER: US 60/121,787  
TITLE OF INVENTION: Novel Component of von Hippel-Lindau Tumor Suppressor  
TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase  
FILE REFERENCE: 021044-004600US  
CURRENT APPLICATION NUMBER: WO PCT/US00/04838  
CURRENT FILING DATE: 1999-02-26  
PRIOR APPLICATION NUMBER: WO PCT/US00/04838  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO: 3  
LENGTH: 508  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (7)..(333)  
OTHER INFORMATION: Rbx1  
US-10-913-937-3

Alignment Scores:  
Pred. No.: 1.08e-110 Length: 508  
Score: 108.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 8 Gaps: 0  
DB: DB:

US-09-541-462B-2 (1-108) × US-10-913-937-3 (1-508)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20  
Db 7 ATGGCCGGAGCGAGGATCTGGATACGGCAACAGGGCAGGGAGGGAG 66  
Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeutTpAlaTrpAspIleValValAsp 40  
Db 67 CGCTTGAACTGTAAGAAAAGTGAATGCACTGGCCCTCTGGCTGGATAATGCTGTTGAT 126  
Qy 41 AsnCysAlaLysCysArgAsnHisIleMetAspLeuCysTrpGlyCysGlnAlaAsnGln 60  
Db 127 AACGTGCCATCTGGAGGACCAATTAGGATCTTGTGATAGATGTCAGTACCGAC 186  
Qy 61 AlaSerAlaThrSerGluCysTrpGlyValCysAsnHisAlaPheHis 80  
Db 187 GCGTCAGCTACTCCAAAGACTGTAGATGGCAACAGTGCTCAAACAGAGAG 246  
Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
Db 247 TTCACTGATCTCTGCTGGCTCAAACAGAGAG 330  
Qy 101 TrpGluPheGlnLysLysTyrGlyHis 108  
Db 307 TGGAAATTCCAAGATGGCAC 330

RESULT 13  
US-10-242-535A-46292  
Sequence 4692, Application US/10242535A  
Publication No. US200401363A1  
GENERAL INFORMATION:  
APPLICANT: ChondroGene Inc.  
APPLICANT: Liwei, C.C.  
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
FILE REFERENCE: 4231/2005  
CURRENT APPLICATION NUMBER: US/10/242,535A  
CURRENT FILING DATE: 2002-09-12  
PRIOR APPLICATION NUMBER: US 10/085,783  
PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340  
 i PRIOR FILING DATE: 2001-07-13  
 i PRIOR APPLICATION NUMBER: US 60/275,017  
 i PRIOR FILING DATE: 2001-03-12  
 i PRIOR APPLICATION NUMBER: US 60/271,955  
 i PRIOR FILING DATE: 2001-02-28  
 i NUMBER OF SEQ ID NOS: 58994  
 i SOFTWARE: PatentIn version 3.2  
 i SEQ ID NO: 46292  
 i LENGTH: 523  
 i TYPE: DNA  
 i ORGANISM: Human  
 US-10-242-535A-46292

Alignment Scores:  
 Pred. No.: 1.11e-110 Length: 523  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-085-783A-46292 (1-523)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyAlaGlyLys 20  
 Db 19 ATGGCGCAGGTGGATGGATGCTGATACCCGAGGGACCAACAGCGGGCGGGCAAGAAG 78

Alignment Scores:  
 Pred. No.: 1.11e-110 Length: 523  
 Score: 108.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 7 Gaps: 0

US-09-541-462B-2 (1-108) x US-10-242-535A-46292 (1-523)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyAlaGlyLys 20  
 Db 19 ATGGCGCAGGTGGATGGATGCTGATACCCGAGGGACCAACAGCGGGCGGGCAAGAAG 78

Qy 21 ArgPheGluValLysTrpAsnAlaValLeuTrpAlaTrpAspIleValAsp 40  
 Db 79 CGCTTAAAGTGAAGAAAGTGGAAAGTGCTGGATATTGGTTGAT 138

Qy 41 AsnCysAlaLeuCysArgAsnHisIleMetAspLeuCysIleGlucysGlnAlaAsnGln 60  
 Db 139 AACTGCCCCATCTGAGAACCATTTGATGTCAGCTTACAG 198

Qy 61 AlaSerAlaThrSerGluGlyCysThrValAlaTrpGlyAlaGlyLys 80  
 Db 199 GCGTCGGCTACTCTGAAAGAGTGTACTGTGTCATGGGAGTCGTAACCATGCTTTCAC 258

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspArgGlu 100  
 Db 259 TTCCACTGCATCTCTGGCTCCATGGACAAACAGGAGTCATGGCTGGATATTGGTTGAT 138

Qy 101 TrpGluPheGlnLysTrpGlyHis 108  
 Db 319 TGGGATTCCTAAAGATGGCAC 342

RESULT 15  
 US-09-918-995-17191  
 i Sequence 17191, Application US/09918995  
 i Publication No. US20030073623A1  
 i GENERAL INFORMATION:  
 i APPLICANT: Hyseq, Inc.  
 i TITLE OF INVENTION: NOVEL NUCLEARIC ACID SEQUENCES OBTAINED  
 i FROM VARIOUS cDNA LIBRARIES  
 i FILE REFERENCE: 20411-756  
 i CURRENT APPLICATION NUMBER: US/09/918,995  
 i CURRENT FILING DATE: 2001-07-30  
 i PRIORITY APPLICATION NUMBER: US/09/235,076  
 i NUMBER OF SEQ ID NOS: 38054  
 i SOFTWARE: FastSEQ for Windows Version 3.0  
 i SEQ ID NO: 17191  
 i LENGTH: 476  
 i TYPE: DNA  
 i ORGANISM: Homo sapiens  
 i FEATURE:  
 i NAME/KEY: misc\_feature  
 i LOCATION: (1)..(476)  
 i OTHER INFORMATION: n = A,T,C or G

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspArgGlu 100  
 Db 259 TTCCACTGCATCTCTGGCTCCATGGACAAACAGGAGTCATGGCTGGATATTGGTTGAT 138

Qy 101 TrpGluPheGlnLysTrpGlyHis 108  
 Db 319 TGGGATTCCTAAAGATGGCAC 342

RESULT 14  
 US-10-085-783A-46292  
 i Sequence 46292, Application US/10085783A  
 i GENERAL INFORMATION:  
 i APPLICANT: ChondroGene Inc.  
 i APPLICANT: Liow, C.C.  
 i TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 i FILE REFERENCE: 4231/2002  
 i CURRENT APPLICATION NUMBER: US/10/085,783A  
 i CURRENT FILING DATE: 2002-02-28  
 i PRIOR APPLICATION NUMBER: US 60/305,340  
 i PRIOR FILING DATE: 2001-07-13  
 i PRIOR APPLICATION NUMBER: US 60/275,017  
 i PRIOR FILING DATE: 2001-03-12  
 i PRIOR APPLICATION NUMBER: US 60/271,955  
 i PRIOR FILING DATE: 2001-02-28  
 i NUMBER OF SEQ ID NOS: 58994  
 i SOFTWARE: PatentIn version 3.2  
 i SEQ ID NO: 46292  
 i LENGTH: 523  
 i TYPE: DNA  
 i ORGANISM: Human  
 US-10-085-783A-46292

Qy	22	PheGluValLysTrpAsnAlaValAlaLeuTrpAlaIleTrpAspIleValAspAsn	41
Db	135	TTTGAAGTGAAAATGGATGCTGGATATGGTGTGATAAC	194
Qy	42	CysAlaIleCysArgAsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAla	61
Db	195	TGTGCCATTGCAAGAACCCATTATGGATCTTGCAAGAATCTAACCTAACAGCG	254
Qy	62	SerAlaIthrSerGluCysSerValAlaIleTrpGlyValCysAsnHisAlaPheHis	81
Db	255	TCCGCTACTTCAGAGAGCTACTGCTGATGGGAGCTGTAAACCARGCTTTCACTTC	314
Qy	82	HisCysIleSerArgTripleLysThrArgGlnValCysProLeuAspAsnArgGluIrp	101
Db	315	CACTGCATTCAGAGAGCTACTGCTGATGGGAGCTGTAAACCARGCTTTCACTTC	374
Qy	102	GluPheGlnLysTyrGlyHis	108
Db	375	GAATTCCAAAAGTAGGGCAC	395

Search completed: March 11, 2006, 10:04:09  
 Job time : 655 secs

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 11, 2006 08:30:45 ; Search time 494 Seconds  
(without alignments)

Scoring table: OLIGO  
Xgapop 60.0 , Xgapext 60.0  
Ygapop 60.0 , Ygapext 60.0  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4996397 seqs, 3332346308 residues

Word size: 12

Total number of hits satisfying chosen parameters: 95

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:

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-Q=/abs/ABSSNBB/sppol/US0911452/runat_10032006_080830_22345/app_query.fasta_1
-DB=N_Geneseq -QFORMAT=fasta -SUFFIX=oligo.rng -MINMATCH=0.1 -LoopCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40_cdi
-LIST=45 -DOCALLIGN=20 -THR SCORE=quality -THR MIN=12 -ALIGN=15 -MODDB=LOCAL
-OUTFORMAT=proto -NORM=ext -HEAPSIZEB=500 -MINLEN=0 -MAXLEN=0 -HOST=abs03h
-USER=US0911452 @CCN 1.1 727 @runat 10032006 080830_22345 -NCPU=6 -TCPU=3
-NO_MMAPP -NEG SCORES=0 -WAIT -DSBLOCK=10 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=10 -THREADS=1 -XGAPOP=60 -XGAPEXT=7 -FGAPEXT=60 -FGAPEXT=7
-YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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Database : N\_Geneseq.21:\*

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- 2: geneseqn1990s:\*
- 3: geneseqn2000s:\*
- 4: geneseqn2001as:\*
- 5: geneseqn2001bs:\*
- 6: geneseqn2002as:\*
- 7: geneseqn2002bs:\*
- 8: geneseqn2003as:\*
- 9: geneseqn2003bs:\*
- 10: geneseqn2003cs:\*
- 11: geneseqn2003ds:\*
- 12: geneseqn2004as:\*
- 13: geneseqn2004bs:\*
- 14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	108	100.0	327	3	AAA96882	Aaa96882 Nucleotid
2	108	100.0	482	3	AAA96886	Aac03896 Human sec
3	108	100.0	504	3	AAA74780	Aaa74780 DNA encod
4	108	100.0	506	12	ADQ87496	Adq87496 Human tum

## ALIGNMENTS

RESULT 1  
ID AAA96882 standard; DNA; 327 BP.  
XX  
AC AAA96882;  
XX DT 19-FEB-2001 (first entry)  
XX DE Nucleotide sequence of human ring finger protein ROC1.  
XX KW ROC1; ROC2; cullin; ring finger protein; APC11; APC complex; SCF pathway;  
KW cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation;  
KW tumour; ss.  
XX OS Homo sapiens.  
XX PN WO200058472-A2.  
FH Key CDS  
FT FT  
FT /\*tag= "ROC1"  
/product= "ROC1"

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	108	100.0	327	3	AAA96882	Aaa96882 Nucleotid
2	108	100.0	482	3	AAA96886	Aac03896 Human sec
3	108	100.0	504	3	AAA74780	Aaa74780 DNA encod
4	108	100.0	506	12	ADQ87496	Adq87496 Human tum

ACN4951\_Tumour-a

Ach29979\_Human tes

Ado89913\_Human the

Acn90161\_Breast ca

Adq92179\_Human aut

Aah97860\_Murine 7-

Aah97862\_Murine 7-

Abv25615\_Human pro

Ac15742\_Human col

Adf42703\_Human Tes

Adq80865\_Human SPA

Aab94844\_Human DNA

Abx39512\_Bovine ES

Aadi12859\_Human nov

Ab122527\_Drosophil

Aac57009\_Pinus rad

Adk56883\_Plant DNA

Adk56888\_Plant DNA

Adk56882\_Plant DNA

Adk56897\_Plant ful

Adk56879\_Plant DNA

Aeb66106\_Rice geno

Adk56881\_Plant DNA

Ady78665\_Human cDN

Abq85150\_Arabidops

Acn5764\_Cotton an

Adr5906\_Cotton CD

Aac39854\_Arabidops

Adr61971\_Cotton CD

Aas86845\_DNA encod

Adk56887\_Plant DNA

Adk56880\_Plant DNA

Ab122526\_Drosophil

Adg99381\_Kidney di



Db 329 TGGAAATCCAAAAGTATGGCAC 352  
**RESULT 3**  
 AAA74380  
 ID AAA74380 standard; DNA; 504 BP.  
 XX  
 AC AAA74380;  
 XX DT 02-JAN-2001 (first entry)  
 XX DE DNA encoding a murine culin-interacting RING-H2 finger protein (Rbx1).  
 XX  
 KW Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1;  
 tumour suppressor; carcinoma; Ring box associated carcinoma;  
 KW von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;  
 KW cerebellar hemangioblastoma; hemangioma; retinal angioma;  
 KW pheochromocytomas; ss.  
 XX OS Mus sp.  
 XX PN WO20050445-A1.  
 XX PD 31-AUG-2000.  
 XX PF 25-FBB-2000; 2000WO-US004838.  
 XX PR 26-FEB-1999; 99US-0121737P.  
 XX PA (OKLA) OKLAHOMA MEDICAL RES FOUND.  
 XX PI Conaway JA, Conaway RC, Kamura T;  
 XX DR WPI; 2000-572067/53.  
 XX PT Cullin interacting RING-H2 finger protein, a component of von Hippel-  
 PT Lindau tumor suppressor complex and Skp1-Cdc33p-F-box protein (SCF)  
 PT ubiquitin ligase, useful for diagnosing and treating Ring box  
 PT associated carcinomas.  
 XX PS Disclosure; Page 35; 37pp; English.  
 XX CC The present sequence encodes a murine cullin-interacting RING-H2 finger  
 CC protein (Ring box protein), designated Rbx1. The human Rbx1 polypeptide  
 CC is a tumour suppressor. Human Rbx1 is useful for diagnosing a  
 CC predisposition of a patient to certain carcinomas. It is also useful for  
 CC treating Ring box protein associated carcinomas or augmenting  
 CC metabolically deficient system in animals. Human Rbx1 is also useful for  
 CC evaluating the effectiveness of a therapeutic treatment for Ring box  
 CC associated carcinomas. Human Rbx1 can be used to screen for agent which  
 CC augment or inhibit the activity of other cullin-containing ubiquitin  
 CC ligase and of the VHL (von Hippel-Lindau) complex controlling the  
 CC conjugation of ubiquitin or ubiquitin-like proteins to various sets of  
 CC target proteins. Carcinomas which may be treated include renal  
 CC carcinomas, cerebellar hemangioblastomas and hemangiomas, retinal  
 CC angioma and pheochromocytomas.  
 XX SQ Sequence 504 BP; 117 A; 107 C; 137 G; 143 T; 0 U; 0 Other;

Alignment Scores:	Length:	504
Pred. No.:	Matches:	108
Score:	Conservative:	0
Percent Similarity:	Mismatches:	0
Best Local Similarity:	Indels:	0
Query Match:	Gaps:	0
DB:		

US-09-541-462B-2 (1-108) x AAA74980 (1-504)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20  
 18 ATGGCGGGATGATGATGCCACACAGCGGGCAAGAG 77  
 Db

Qy 21 ArgPheGluValLysSlySTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValValAsp 40  
 78 ccCTTGAAAGTTAAAGATGGCACATTGGTTGAT 137  
 Db 41 AsnCysAlaIleCysArgAspHisIleMetAspLeuCysIleGluCysGlnAlaAsnGln 60  
 138 AACCTGRCGCATCTGGCAACACATTGGATCTTGATGAACTGGCACCAG 197  
 Qy 61 AlaSerAlaThrSerGluCysIleSerValAlaTrpGlyValCysAsnHisAlaPheHis 80  
 Db 198 GCGTCAGCTACTTCGAAGAGTGTACGGTTCGATGGAGTCGACCATGCTTTCAT 257  
 Qy 81 PheHisCysIleSerArgTrpLeuIysThrArgGlnValCysProlIeuAspAsnArgGlu 100  
 Db 258 TTCCACTGCAVCTCTGATGCTCAAACGGGCAAGTGTGAGAACAGAG 317  
 Qy 101 TrpGluPheGlnIlysTrpGlyHis 108  
 Db 318 TGGGACTTCGGAAGTAGATGGCCAT 341

**RESULT 4**  
 ADQ87496  
 ID ADQ87496 standard; cDNA; 506 BP.  
 XX  
 AC ADQ87496;  
 XX DT 07-OCT-2004 (first entry)  
 XX Human tumour-associated antigenic target (TAT) cDNA sequence #4374.  
 DE XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
 KW cancer; cell proliferative disorder; gene; ss.  
 XX OS Homo sapiens.  
 XX PN WO2004060270-A2.  
 XX PD 22-JUL-2004.  
 XX PP 15-OCT-2003; 2003WO-US029126.  
 XX PR 18-OCT-2002; 2002US-0418988P.  
 XX PA (GETH ) GENENTECH INC.  
 PA (WITD/) WU T D.  
 PA (ZHOU/) ZHOU Y.  
 XX PI Wu TD, Zhou Y;  
 XX DR WPI; 2004-534300/51.  
 XX PS Claim 1; SEQ ID NO 4374; 5504pp; English.  
 XX CC The present invention describes an isolated tumour-associated antigenic  
 CC target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide  
 CC sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of  
 CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%  
 CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-  
 CC (c). Also described: (1) an expression vector comprising the above  
 CC nucleic acid; (2) a host cell comprising the above expression vector; (3)  
 CC a process for producing a polypeptide; (4) an isolated polypeptide  
 CC comprising: (a) an amino acid sequence encoded by any of the above  
 CC nucleotide sequences; (b) an amino acid sequence encoded by the full-  
 CC length coding region of the above nucleotide sequences; or (c) a sequence  
 CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide  
 CC comprising the above polypeptide fused to a heterologous polypeptide;  
 CC an isolated antibody that binds to the above polypeptide; (7) a process  
 CC for producing the antibody; (8) an isolated oligopeptide that binds to  
 CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)  
 CC binding organic molecule that binds to the above polypeptide; (10) a

composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

XX Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

SQ Alignment Scores:  
Pred. No.: . 2.73e-106 Length: 506  
Score: 108.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indexes: 0  
DB: 12 Gaps: 0

US-09-541-462B-2 (1-108) × ADQ87496 (1-506)

QY 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysIys 20  
6 ATGGCCGACGGATCGATGCTGGATACTCCCAAGGCCACCCAAAGGGCCGGGAAAGAG 65  
QY 21 ArgPheGluValIleIleTrpAsnAlaValAlaLeuTyrTyrPheValAlaAsp 40  
66 CGCTTGAACTGTGAAAAGTGAATCGAATCGACGCCCCCTGGATATGTCGGTTGAT 125  
QY 41 AsnCysAlaLeuCysArgAsnHist1LeuAspLeuCysteGluCysGlnAlaAsnGln 60  
126 AACTGCCCATCTGAGGACCAATTGATCTGATAGATGTAAGCTAACACAG 185  
QY 61 AlaSerAlaThrSerGluGlyCysThrValAlaTyrGlyValCysAsnHisAlaPheHis 80  
186 GCGTCCGCTACTTCACAAGCTGTACTGTCGCCTGTCACGTTCACTGCTTA 245  
QY 81 PheHisCysIleSerArgTrpLeuIleThrArgGlnValcysProLeuAspIleAspArg 100  
Db 246 TTCCACTGCATCTCTGGCTCAAAACGACAGGTGTCATGGCACAACTGACAGAG 305  
QY 101 TrpGluPheGlnLysItyArgIlyHis 108  
Db 306 TGGGAATTCAAAAGTATGGGCAC 329

RESULT 5  
ID ADQ87156 standard; cDNA; 506 BP.  
XX AC ADQ87156;  
XX DT 07-OCT-2004 (first entry)  
XX DE Human tumour-associated antigenic target (TAT) cDNA sequence #4032.  
XX KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;  
KW cancer; cell proliferative disorder; gene; ss.  
XX OS Homo sapiens.

PN WO2004060270-A2.  
XX PD 22-JUL-2004.

XX PF 15-OCT-2003; 2003WO-US029126.

XX PR 18-OCT-2002; 2002US-0418988P.

XX PA (GENTECH INC.  
(GENTECH ) GENENTECH INC.  
(WTDD/ ) WU T D.  
(Zhou/ ) ZHOU Y.  
XX PA  
XX PI Wu TD, Zhou Y;  
XX DR WPI; 2004-534300/51.

XX PT New nucleic acid molecule and encoded polypeptide, for diagnosing,  
PT preventing or treating cell proliferative disorders such as cancer.  
XX PS Claim 1; SEQ ID NO 4032; 5504pp; English.  
XX CC The present invention describes an isolated tumour-associated antigenic

CC target (TAT) nucleic acid comprising: (a) any of 462 nucleotide

CC sequences (see SEQ ID NO:1 to 462); (b) the full-length coding region of

CC (a); (c) the complement of (a) or (b); (d) a sequence that has 80%

CC sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-

CC (c). Also described: (1) an expression vector comprising the above

CC nucleic acid; (2) a host cell comprising the above expression vector; (3)

CC a process for producing a polypeptide; (4) an isolated polypeptide

CC comprising: (a) an amino acid sequence encoded by any of the above

CC nucleotide sequences; (b) an amino acid sequence encoded by the full-

CC length coding region of the above nucleotide sequences; or (c) a sequence

CC having at least 80% identical to (a) or (b); (5) a chimeric polypeptide

CC comprising the above polypeptide fused to a heterologous polypeptide; (6)

CC an isolated antibody that binds to the above polypeptide; (7) a process

CC for producing the antibody; (8) an isolated oligopeptide that binds to

CC the above polypeptide; (9) a tumour-associated antigenic target (TAT)

CC binding organic molecule that binds to the above polypeptide; (10) a

CC composition of matter comprising the above (chimeric) polypeptide,

CC antibody, oligopeptide or TAT binding organic molecule, in combination

CC with a carrier; (11) an article of manufacture comprising a container and

CC the composition of matter contained within the container; (12) methods of

CC inhibiting the growth of a cell that expresses the above protein, where

CC the growth of the cell is at least in part dependent upon a growth

CC promoting effect of the above protein; (13) a method of

CC therapeutically treating a mammal having a cancerous tumour comprising

CC cells that express the above protein; (14) a method of determining the

CC presence of a protein in a sample suspected of containing the protein

CC described above; (15) methods of diagnosing the presence of a tumour in a

CC mammal; (16) a method for treating or preventing a cell proliferative

CC disorder associated with increased expression or activity of the above

CC protein; and (17) a method of binding an antibody, oligopeptide or

CC organic molecule to a cell that expresses the protein described above.

CC The TAT sequences have cytostatic activities, and can be used in gene

CC therapy. The composition and methods are useful for diagnosing,

CC preventing or treating cancer. The composition is also used for preparing

CC a medicament for the therapeutic treatment or diagnostic detection of a

CC cell proliferative disorder or cancer. The present sequence represents a

CC human TAT cDNA sequence from the present invention.

XX SQ Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;  
XX Alignment Scores:  
Pred. No.: 2.73e-106 Length: 506  
Score: 108.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indexes: 0  
DB: 12 Gaps: 0

XX Alignment Scores:  
Pred. No.: 2.73e-106 Length: 506  
Score: 108.00 Matches: 108  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 100.0% Indexes: 0  
DB: 12 Gaps: 0

US-09-541-462B-2 (1-108) × ADQ87156 (1-506)

Qy 1 MetalAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysIys

**RESULT 6**

ADQ84881 standard; cDNA; 506 BP.

XX ADQ84881 standard; cDNA; 506 BP.

AC ADQ84881;

XX DT 07-OCT-2004 (first entry)

XX DE Human tumour-associated antigenic target (TAT) cDNA sequence #1695.

XX KW human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.; gene therapy;

XX OS Homo sapiens.

XX PN WO2004060270-A2.

XX PD 22-JUL-2004.

XX PF 15-OCT-2003; 2003WO-US029126.

XX PR 18-OCT-2002; 2002US-041898P.

XX PA (GETH ) GENENTECH INC.

PA (WUTD ) WU T D.

PA (ZHOU /) ZHOU Y.

XX PI Wu TD; Zhou Y;

XX DR WPI; 2004-534300/51.

XX PT New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer.

XX PS Claim 1: SEQ ID NO 1695; 5504pp; English.

XX CC The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full length coding region of (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above nucleotide sequences; (b) an amino acid sequence encoded by the full-length coding region of the above nucleotide sequences; or (c) a sequence having at least 80% identity to (a) or (b); (5) a chimeric polypeptide comprising the above polypeptide fused to a heterologous polypeptide; (6) an isolated antibody that binds to the above polypeptide; (7) a process

CC for producing the antibody; (8) an isolated oligopeptide that binds to the above polypeptide; (9) a tumour-associated antigenic target (TAT) binding organic molecule that binds to the above polypeptide; (10) a composition of matter comprising the above (chimeric) polypeptide, antibody, oligopeptide or TAT binding organic molecule, in combination with a carrier; (11) an article of manufacture comprising a container and the composition of matter contained within the container; (12) methods of inhibiting the growth of a cell that expresses the above protein, where the growth of the cell is at least in part dependent upon a growth potentiating effect of the above protein; (13) a method of therapeutically treating a mammal having a cancerous tumour comprising cells that express the above protein; (14) a method of determining the presence of a protein in a sample suspected of containing the protein described above; (15) methods of diagnosing the presence of a tumour in a mammal; (16) a method for treating or preventing a cell proliferative disorder associated with increased expression or activity of the above protein; and (17) a method of binding an antibody, oligopeptide or organic molecule to a cell that expresses the protein described above. The TAT sequences have cytostatic activities, and can be used in gene therapy. The composition and methods are useful for diagnosing, preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a human TAT cDNA sequence from the present invention.

XX SQ Sequence 506 BP; 126 A; 105 C; 124 G; 151 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No. :	2.73e-106	Length:	506
Score:	108.00	Matches:	108
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	13	Gaps:	0

US-09-541-462B-2 (1-108) x ADQ84881 (1-506)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLys 20

Db 6 ATGGCGCAGCGTAGCGATGGATGGATACCCCGACGGGACCAACAGGGCGGGCAAAG 65

Qy 21 ArgPheGluValLysLysTTPAsnAlaValAlaLeuTTPAlaTrpAspIleValAsp 40

Db 66 CGCTTGAACTGAAAAAAGTGAATTCGAACTTGTGGATATTGGTTGAT 125

Qy 41 AsnCysAlaLysLysCArgAlaHisIleMetAspIeuCysteGluCysGlnAlaLysGln 60

Db 126 AACCTGCCCCATCTGGAAACCACATTAGGATAGTGAATGTCAGCTAACCG 185

Qy 61 AlaSerAlaThrSerGluGluCysSerhrValAlaTrpGlyValCysAsnHisAlaPheHis 80

Db 186 GCGTCGGCTACTTCAGAAGAGTGACTGTGCATGGGACTCTGTAACTATGCTTCAC 245

Qy 81 PheHisCysSerIleSerArgTrpLeuLysThrArgGlnValCysProLeuLysPheAsnArgGlu 100

Db 246 TTCCACTGCAATCTCGCTGGCTAAACACGAACTGGGTCATTGGACAAACAGAGAG 305

Qy 101 TrpGluPheGlnLysThrGlyHis 108

Db 306 TGGAAATTCCAAAAGTATGGGAC 329

RESULT 7

AAA74978 standard; DNA; 508 BP.

XX AC AAA74978;

XX DT 02-JAN-2001 (first entry)

XX DE DNA encoding a human cullin-interacting RING-H2 finger protein (Rbx1).

XX KW Cullin-interacting RING-H2 finger protein; Ring box protein; Rbx1; tumour suppressor; carcinoma; Ring box associated carcinoma;

XX KW

KW von Hippel-Lindau complex; ubiquitin conjugation; renal carcinoma;  
KW cerebellar hemangioblastoma; hemangioma; retinal angioma;  
KW pheochromocytomas; ss.  
XX Homo sapiens.  
XX Location/Qualifiers  
Key CDS 7 .333 /\* tag= a  
FT /product= "cullin-interacting RING-H2 finger protein  
FT (Rbx1)"  
XX WO2000050445-A1.  
XX PD 31-AUG-2000.  
XX PP 25-FEB-2000; 2000WO-US004838.  
XX PR 26-FBB-1999; 9US-0121787P.  
XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.  
XX Conaway JA, Conaway RC, Kamura T;  
PI XX DR WPI: 2000-572067/53.  
DR P-PSDB; AAB08813.  
XX Cullin interacting RING-H2 finger protein, a component of von Hippel-  
Lindau tumor suppressor complex and Skp1-Cdc53p-F-box protein (SCF)-  
ubiquitin ligase, useful for diagnosing and treating Ring box protein  
associated carcinomas.  
XX PS Claim 3; Page 35; 37pp; English.  
XX The present sequence encodes a human cullin-interacting RING-H2 finger  
protein (Ring box protein), designated Rbx1. The polypeptide is a tumour  
suppressor. Rbx1 is useful for diagnosing a predisposition of a patient  
to certain carcinomas. It is also useful for treating Ring box protein  
associated carcinomas or augmenting metabolically deficient system in  
animals. Rbx1 is also useful for evaluating the effectiveness of a  
therapeutic treatment for Ring box associated carcinomas. Rbx1 can be  
used to screen for agents which augment or inhibit the activity of other  
cullin-containing ubiquitin ligase and of the VHL (von Hippel-  
Lindau) complex controlling the conjugation of ubiquitin or ubiquitin-like  
proteins to various sets of target proteins. Carcinomas which may be  
treated include renal carcinomas, cerebellar hemangioblastomas and  
hemangiomas, retinal angioma and pheochromocytomas

Sequence 508 BP, 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;  
XX Alignment Scores:  
Pred. No.: 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerIylAlaGlyLysLys 20  
Score: 7 ATGGCGCAGCATGGATGGATGGATACCCGAGGGACCACAGCGCCGGCAAGAG 66  
Percent Similarity: 100.0% Best Local Similarity: 100.0% Query Match: 100.0% DB:  
Matches: 108.00 Conservatve: 0 Mismatches: 0 Indels: 0 Gaps: 0  
Length: 508

us-09-541-462B-2 (1-108) x AAA714978 (1-508)  
Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerIylAlaGlyLysLys 20  
Db 7 ATGGCGCAGCATGGATGGATGGATACCCGAGGGACCACAGCGCCGGCAAGAG 66  
Qy 21 ArgPheGluValLysIylTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAsp 40  
Db 67 cacttrrAAGTCAAATGGATGGATGGCTGGGCTGGATATGTGGTTATG 126  
Qy 41 AsnCysAlaIleCysArgAsnHisIleMetAspLysIleGluCysGlnAlaLysGln 60  
Db 127 AACTGTCGCCATCTGCAGGAACCATPATGATCATTCAGAAATGCAAGCTAACAG 186  
Qy 61 AlaSerAlaThrSerGluGluCysThrValAlaTrpDlyValCysAsnHisAlaPheHis 80

Db 187 GCCTCCGCTACTTCAGAGGTACTTCAGCTGGAGATCTGTAACATGCTTTTCAC 246  
Qy 81 PheIscysIleSerArgTrpLeuLysThrArgLysProLeuAspAlaArgLysLys 100  
Db 247 TTCACTGCATCTCGCTGGCTAAACACGAGCTGGTCCATTGGACAAACAGAG 306  
Qy 101 TrpGluIlePheGlnIlysTyrglyHis 108  
Db 307 TGCGAATTCCAAGTAGTGGCAC 330  
RESULT 8  
ACN40951 ID ACN40951 standard; cDNA; 508 BP.  
XX ACN40951:  
XX DT 18-NOV-2004 (first entry)  
DE Tumour-associated antigenic target (TAT) cDNA DNA3326980, SEQ ID NO:6072.  
XX Tumour-associated antigenic target; TAT; human; overexpression; cancer;  
KW tumour; diagnosis; cell proliferative disorder; breast cancer;  
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;  
KW central nervous system cancer; bladder cancer; pancreatic cancer;  
KW cervical cancer; melanoma; leukemia; hybridisation probe;  
KW chromosome identification; chromosome mapping; gene mapping;  
KW gene therapy; cytostatic; gene; ss.  
XX Homo sapiens.  
XX WO2004030615-A2.  
PN PN 15-APR-2004.  
XX PD 29-SEP-2003; 2003WO-US028547.  
XX PR 02-OCT-2002; 2002US-0414971P.  
XX PA (GETH ) GENENTECH INC.  
XX PI Wu TD, Zhang Z, Zhou Y;  
XX DR WPI: 2004-347921/32.  
DR P-PSDB; ABM82365.  
XX New tumor-associated antigenic target polypeptides and nucleic acids,  
PT useful in preparing a medicament for treating or detecting a  
PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or  
PT prostate cancer or tumor.  
XX DR 15-APR-2004.  
XX PS Claim 1; SEQ ID NO 6072; 7273pp; English.  
XX The invention relates to human tumour-associated antigenic target ("TAT")  
polypeptides, and their related nucleic acids. The TAT polypeptides are  
overexpressed in cancer tissues compared to normal tissues, and may thus  
serve as effective targets for the diagnosis and treatment of cancer in  
mammals. The invention also relates to nucleic acid and polypeptide  
sequences at least 80% identical to the TAT nucleic acids and  
polypeptides, expression vectors and host cells comprising a TAT nucleic  
acid; an antibody specific for TAT polypeptide; a peptide or organic  
molecule which binds to a TAT polypeptide; fusion proteins comprising a  
TAT polypeptide; and methods and compositions for the treatment or  
diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,  
antibodies, antagonists, binding molecules and compositions are useful  
for diagnosing or treating a cell proliferative disorder associated with  
increased TAT expression, particularly cancers such as breast cancer,  
colon cancer, lung cancer, ovarian cancer, liver cancer, bladder  
cancer, pancreatic cancer, cervical cancer, cancers of the central  
nervous system, melanoma and leukemia. TAT nucleic acids may further be  
used as hybridisation probes, in chromosome and gene mapping, in  
chromosome identification and in gene therapy. The present sequence  
represents a TAT nucleic acid of the invention.

PT antisense DNA or RNA.  
 XX  
 SQ Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;  
 PS Claim 1; SEQ ID NO 17191; 44pp; English.  
 XX  
 Alignment Scores:  
 Precl. No.: 2.74e-106 Length: 508  
 Score: 10.8.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 13 Gaps: 0  
 XX  
 US-09-541-462B-2 (1-108) x ACN40951 (1-508)  
 Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyLysSerGlyLysLysLys 20  
 Ddb 7 ATGGCGCCAGGATGGATGCGATGGATACCCGGGCCACANACAGCGCGCCGAAAG 66  
 Qy 21 ArgPheGluValLysLysTTAAsnAlaValAlaLeuTrpAlaTrpAspIleuValAsp 40  
 Ddb 67 GCGTTGAAGTGAAGAAAGTGGAATGCACTGGATGGCTGGGATATTGTGGTGTAT 126  
 Qy 41 AsnCysAlaLysLysCysArgAsnHisLysIleMetAspLeuCysIleGlucysGlnAlaAsnGln 60  
 Ddb 127 AACATGGCATCTGAGGAACACAAATTGATCATTGATTCATTGATCAGCTAACAG 186  
 Qy 61 AlaserAlaThrSerGluGlyCystarvalAlaTrpGlyValCysAsnHisAlaPheHis 80  
 Ddb 187 CGTCGCGCTACTTCGAAAGGTGATCTGTCATGGGAGTCTGCTAACATGCTTTCAC 246  
 Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Ddb 247 TTCCACTGCATCTCGCTACTCTAACACGACAGCTGTTCCATTGGACAACAGAG 306  
 Qy 101 TrpGluPheGlnLysTyrGlyHis 108  
 Ddb 307 TGGGATTCTAAAATGATGGCAC 330  
 XX  
 RESULT 9  
 ID ACH29979 standard; cDNA: 476 BP.  
 XX  
 ACH29979;  
 Human: 89; sequencing by hybridisation, SBH, expressed sequence tag; EST; genome mapping; biodiversity; genetic disorder.  
 Homo sapiens  
 US2003073623-A1.  
 PD 17-APR-2003.  
 XX  
 PF 30-JUL-2001; 2001US-00918995.  
 PR 30-JUL-2001; 2001US-00918995.  
 PA (DRMANAC R.T.)  
 PA (LABA/LABAT I.)  
 PA (STAC/STACHE-CRAIN B.)  
 PA (DICK/DICKSON M.C.)  
 PA (JONE/JONES L.W.)  
 XX  
 PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW,  
 XX  
 WPI; 2003-615964/58.  
 PT New polynucleotide sequences obtained from various cDNA libraries, useful  
 PT as hybridization probes, as oligomers for PCR, for chromosomal or gene mapping,  
 PT mapping, in the recombinant production of protein, or in generating  
 XX Human therapeutic DNA - SEQ ID 150.  
 ID ADS0913/C  
 XX ADS0913 standard; DNA; 3726 BP.  
 AC ADS0913;  
 XX  
 DT 16-DEC-2004 (first entry)  
 DE Human inflammatory; antianemic; cytostatic; vulnerary;  
 KW inflammatory; haematoxisis; immunity; neurodegenerative stem cell;  
 KW aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.  
 OS Homo sapiens.



Db 845 TGCAATCTCTGGCTAAAAACAGCACGGTGTCCATTGACACAGAGTGAA 786  
 Qy 103 PheGlnIstyCylHs 108  
 Db 785 TTCCAAAAGTATGGCAC 768

RESULT 12  
 ADDQ92179  
 ID ADDQ92179 standard; DNA; 503 BP.  
 XX ADQ92179;  
 AC 07-OCT-2004 (first entry)

DE Human autoantigen DNA fragment MPMG#8001L05536.  
 XX ds; autoantigen; antibody; hybridoma; biosensor chip;  
 XX extracorporeal differential diagnosis; autoimmune disease;  
 KW ribosomal protein; tubulin;  
 KW dolichyl-di-phospho-oligosaccharide-glycosyl transferase;  
 KW multiple sclerosis; rheumatoid arthritis; epitope mapping;  
 KW affinity chromatography; electrophoresis; autogambody apheresis;  
 KW RNA interference; RNAi.  
 XX Homo sapiens.  
 XX WO2004058972-A1.  
 XX PD 15-JUL-2004.  
 XX PF 23-DEC-2002; 2002WO-EP014731.  
 XX FR 23-DEC-2002; 2002WO-EP014731.  
 XX PA (THIE-) THIESSEN H.  
 XX PA (LORENZ) LORENZ F.  
 PI Thiessen H., Lorenz P;  
 XX DR WPI; 2004-543459/52.  
 XX PT New human DNA autoantigens, useful as assay, diagnostic, and prognostic  
 PT reagents and for treating autoimmune disease, also related expression  
 PT products and antibodies with similar uses.  
 XX PS Claim 1; SEQ ID NO 160; 110pp; German.  
 XX CC This invention describes novel human DNA autoantigens which are used to  
 CC produce recombinant expression vectors; prokaryotic or eukaryotic cells;  
 CC poly- or mono-clonal antibodies (Ab); specific; hybridomas that express  
 CC monoclonal Ab; biosensor chips having an addressable sequence pattern as  
 CC probe; medical or diagnostic instruments that include the biosensor; for  
 CC extracorporeal differential diagnosis of autoimmune diseases and  
 CC predisposition to them. The autoantigens are polynucleotides encode ribosomal  
 CC proteins; tubulins; dolichyl-diphospho-oligosaccharide-glycosyl  
 CC transferases and proteins. The antibodies may be labelled conventionally  
 CC with radioisotopes, coloured or fluorescent groups, or a member of the  
 CC biotin/avidin pair, or colloidal gold. The autoantigens can be directed  
 CC against mitochondria, liver-kidney microsomes; histidine-tRNA; nuclear  
 CC membrane; neutrophilin/cytoplasm; insect cells; epidermal intracellular  
 CC or basal membrane antigens; Golgi or cell nuclei, or associated with  
 CC multiple sclerosis or rheumatoid arthritis. They are useful for epitope  
 CC mapping; in affinity chromatography or electrophoresis; for diagnosis,  
 CC prognosis, control of treatment or therapeutic response of autoimmune  
 CC diseases, particularly in vitro differential diagnosis of autoimmune  
 CC diseases; to produce biosensor chips or for antibody apheresis.  
 CC Autoantigen DNA can be used for therapeutic RNA interference against  
 CC autoantibodies. Biochips that carry the new materials are useful in  
 CC medical and diagnostic instruments. ADDQ92179-ADQ92280 represent human  
 CC autoantigens.  
 XX Sequence 503 BP; 131 A; 102 C; 120 G; 150 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 4.47e-103 Length: 503  
 Score: 105.00 Matches: 105  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 97.2% Indels: 0  
 DB: 12 Gaps: 0

US-09-541-462B-2 (1-108) x ADDQ92179 (1-303)

Qy 4 AlaMetAspPvalAspThrProSerGlyThrAsnSerGlyAlaGlyIleSlyArgPheGlu 23  
 Db 3 GCGATGGATGTGGATACCCCGAGCGGACCAAAGGGCAGAAGCGCTTGAA 62

XX 24 ValLysIstPsaAlaValAlaLeuTrpAlaLysPaspIleValLysAsnCysAla 43  
 Db 63 GAGAAAGATGGATCAGTAGGCCCTGGCCCTGGATAATGGCTTGTATACTGCC 122

Qy 44 IleCysArgArgNH2IleMetAspLeuCysIleGluCysGlnAlaLysGlnAlaSerAla 63  
 Db 123 ATCTGGAGGAACCACATTATGCATAGATGTCAGCTAACAGCTAACAGGGCTCGCT 182

Qy 64 ThrsArgLysGluCysThrValAlaTrpGlyAlaValCysAsnHisAlaAspHeHiScys 83  
 Db 183 ACTTCGAAAGAGTGTACTGTCGATGGGAGTCAGTTTCACTTCCTACTGC 242

Qy 84 IleSerArgTrpLeuLysThrArgGlnValCysProLeuLysAspArgGluTrpGluPhe 103  
 Db 243 ATCTTCGCTGGCTCAAAACAGCACAGGCTCATGGTACAGACTGGGATTC 302

Qy 104 GluLysIstGlyHis 108  
 Db 303 CAAACTATGGCAC 317

RESULT 13  
 AAH97860 standard; DNA; 539 BP.  
 ID AAH97860 XX  
 XX AAH97860 XX  
 AC AAH97860; XX  
 XX DT 10-OCT-2001 (first entry)  
 DE Murine 7-transmembrane G-protein coupled receptor coding sequence #104.  
 XX KW Murine; hematopoietic stem cell; signalling; vaccine; 7TM-GPCR;  
 KW 7-transmembrane G-protein coupled protein receptor; ds;  
 XX OS Mus sp.  
 XX WO200160999-A1.  
 PN XX  
 XX 23-AUG-2001.  
 PD XX  
 XX 14-FEB-2001; 2001WO-US004700.  
 PP XX  
 XX 14-FEB-2000; 2000US-0183377P.  
 PR XX  
 XX (IMCL-) IMCLONE SYSTEMS INC.  
 PA XX  
 PA (UPR-) UNIV PRINCETON.  
 XX PI Lemischka IR, Witte L, Pereira DS;  
 XX DR WPI; 2001-522396/57.  
 XX  
 PT DNA sequences encoding 7-transmembrane G-protein coupled protein  
 PT receptors characteristic of hematopoietic stem cells, useful for treating  
 PT leukemia.  
 XX  
 PS Claim 1; Page 62; 176pp; English.  
 XX  
 CC The present invention relates to murine coding sequences for 7-  
 CC transmembrane G-protein coupled protein receptors (7TM-GPCRs). The  
 CC transmembrane G-protein coupled protein receptors (7TM-GPCRs). The

present sequence is one such murine 7TM-GPCR coding sequence. The present sequence was derived from hematopoietic stem cells. The present sequence and its corresponding protein are useful in the prevention, diagnosis and treatment of diseases associated with inappropriate 7TM-GPCR expression. 7TM-GPCRs identify specific signalling molecules, to activate an effector -signalling cascade that triggers an intracellular response and eventually a biological effect.

XX Sequence 539 BP; 128 A; 112 C; 150 G; 149 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 4 4.77e-103 Length: 539  
Score: 105.00 Matches: 105  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 97.2% Indels: 0  
DB: 5 Gaps: 0

US-09-541-462B-2 (1-108) x AAH97860 (1-539)

QY 4 AlaLeuAspAlaAspThrProSerGlyAlaGlyLysIleAspPheGlu 23  
Db 1 GCGATGGATGGATAACCCCCAGGGCACCAACACGGGGCCAAAGGGCTTCAA 60

QY 24 ValIlysLysTrpAsnAlaValAlaLeuTrpAlaIleLeuTrpAspIleValAspAsnCysAla 43  
Db 61 GTTAAAATGGAAATGGCAAGGGCCCTCTGGCCTGGACATTGGCTGATAACTGICC 120

QY 44 IleCysArg9AsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAla 63  
Db 121 ATCTGAGAACCATATTGGATCTTGTATCGATGTCAGGCCAACAGGCCCTCAACT 180

QY 64 ThrSerGluGluCysThrValIalTrpGlyIvalCysAsnHisAlaPheHisIleHis 83  
Db 181 ACTCGAAGGTGACGGTTGATGGGATGGCTGCACCATGCTTCTATTCACGCC 240

QY 84 IleSerArgTrpLeuLysThrArgInValCysProLeuAspAsnArgGluTrpGlutPhe 103  
Db 241 ATCTCTGATGGCTCAAACGAGGAGGTGTCGTTGJGACARAGAGTGAGFTIC 300

QY 104 GluIlysTrpGlyHis 108  
Db 301 CAGAACTATGGCAT 315

RESULT 14  
AAH97862  
ID AAH97862 standard; DNA; 586 BP.

XX AC AAH97862;

XX DT 10-OCT-2001 (First entry)

DB Murine 7-transmembrane G-protein coupled receptor coding sequence #106.

XX KW Murine; hematopoietic stem cell; signalling; vaccine; 7TM-GPCR;  
KW 7-transmembrane G-protein coupled protein receptor; ds.

XX OS Mus sp.

XX PN WO200160999-A1.

XX PD 23-AUG-2001.

XX PF 14-FEB-2001; 2001WO-US004700.

XX PR 14-FEB-2000; 2000US-0182377P.

XX (IMCL ) IMCLONE SYSTEMS INC.

PA (UYPR ) UNIV PRINCETON.

XX PI Lemischka IR, Witte L, Pereira DS;

XX DR WPI; 2001-522596/57.

XX DNA Sequences encoding 7-transmembrane G-protein coupled protein receptors characteristic of hematopoietic stem cells, useful for treating leukemia.

XX Claim 1; Page 63; 176pp; English.

XX The present invention relates to murine coding sequences for 7-transmembrane G-protein coupled protein receptors (7TM-GPCRs). The present sequence is one such murine 7TM-GPCR coding sequence. The present sequence was derived from hematopoietic stem cells. The present sequence and its corresponding protein are useful in the prevention, diagnosis and treatment of diseases associated with inappropriate 7TM-GPCR expression. 7TM-GPCRs identify specific signalling molecules, to activate an effector -signalling cascade that triggers an intracellular response and eventually a biological effect.

XX Sequence 586 BP; 140 A; 122 C; 164 G; 159 T; 0 U; 1 Other;

SQ Alignment Scores:  
Pred. No.: 5.15e-103 Length: 586  
Score: 105.00 Matches: 105  
Percent Similarity: 100.0% Conservative: 0  
Best Local Similarity: 100.0% Mismatches: 0  
Query Match: 97.2% Indels: 0  
DB: 0 Gaps: 0

US-09-541-462B-2 (1-108) x AAH97862 (1-586)

QY 4 AlaMetAspValAspThrProSerGlyAlaGlyLysIleAspPheGlu 23  
Db 1 GCGATGGATGGATAACCCCCAGGGCACCAACACGGGGCCAAAGGGCTTCAA 60

QY 24 ValIlysLysTrpAsnAlaValAlaLeuTrpAlaIleLeuTrpAspIleValAspAsnCysAla 43  
Db 61 GTTAAAATGGATGGCTGAGTCAGTGGCTGAGTCAGTGGCTGATAACTGTCGC 120

QY 44 IleCysArg9AsnHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAla 63  
Db 121 ATCTGAGAACCATATTGGATCTTGTATCGATGTCAGGCCAACAGGCCCTCAACT 180

QY 64 ThrSerGluGluCysThrValIalTrpGlyIvalCysAsnHisAlaPheHisIleHis 83  
Db 181 ACTCGAAGGTGACGGTTGATGGGATGGCTGCACCATGCTTCTATTCACGCC 240

QY 84 IleSerArgTrpLeuLysThrArgInValCysProLeuAspAsnArgGluTrpGlutPhe 103  
Db 241 ATCTCTGATGGCTCAAACGAGGAGGTGTCGTTGJGACARAGAGTGAGFTIC 300

QY 104 GluIlysTrpGlyHis 108  
Db 301 CAGAACTATGGCAT 315

RESULT 15  
ABV25615/C  
ID ABV25615 standard; cDNA; 4476 BP.

XX AC ABV25615;

XX DT 16-SEP-2002 (first entry)

XX DE Human prostate expression marker CDNA 25606.

XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker;

XX XX pharmacogenomic marker; gene; ss.

OS Homo sapiens.

XX WO200160860-A2.

XX XX

XX PD 23-AUG-2001.

XX XX

XX PR 20-FEB-2001; 2001WO-US005171.

XX PF 20-FEB-2001.

XX  
 PR 17-FEB-2000; 2000US-0183319P.  
 PR 16-MAR-2000; 2000US-0189862P.  
 PR 23-MAY-2000; 2000US-0207454P.  
 PR 09-JUN-2000; 2000US-0211314P.  
 PR 18-JUL-2000; 2000US-0219007P.  
 PR 13-DEC-2000; 2000US-0255281P.  
 XX  
 PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX  
 PI Schlegel R, Endge WO, Monahan JE;  
 XX DR WPI: 2001-662795/76.

XX PT Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.

XX PS Claim 1; Page 5119-5120; 11750pp; English.

XX CC The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient; (d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a patient; (I) is also useful as a pharmacodynamic or pharmacogenomic marker

XX SQ Sequence 4476 BP; 1085 A; 1129 C; 1015 G; 1247 T; 0 U; 0 Other;

Alignment Scores:	Length:
Pred. No.: 4.75e-100	4476
Score: 103.00	Matches: 103
Percent Similarity: 100.0%	Conservative: 0
Best Local Similarity: 100.0%	Mismatches: 0
Query Match: 95.4%	Indels: 0
DB: 5	Gaps: 0

US-09-541-462B-2 (1-108) x ABV25615 (1-4476)

Qy	Aa	Alignment Scores:	Length:
Db	AlaAlaLysAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysLysAspArgPhe	22	
Db	1014 GCAGCGATGGATGGTGTGATACCCGGGGCACAAAGCGGGCGGCCAAGGCCCTTT	955	
Qy	23 GluValLysLysTTpanAlaValAlaLeuTrpAlaTrpAspIleValAspAsnCys	42	
Db	954 GAA GTG AAA ACT GG AA GTG CAG TA GG CCT CT GG CT GG AT ATT TT GG T GT GATAACT GT	895	
Qy	43 AlaIleSerArgAsnHisIleMetAspLeuCysIleLysGlnAlaAsnGlnAlaser	62	
Db	894 GCCATCTCGAGAACCCATATTGGATTCATAGCAATGTCAGCTAACGGGTCC	835	
Qy	63 AlaThrSerGluGluCysThrValAlaTrpGlyIvaIcyAsnHisAlaPheHisPheHis	82	
Db	834 GCTACTTCAGAGAGTGTACTCTCGATGGGAAGTGTAACCATTCTTCACITCCAC	775	
Qy	83 CysIleSerArgTriplolySThrArgGlnValCysProLeuAspAsnA9GluTrpGlu	102	
Db	774 TSCATCTCTCGTGGCTCAAACACGCAAGGTGTGTCATTTGGACAAAGAGTGGAA	715	
Qy	103 PheGlnIby 105		
Db	714 TTCCAAA 706		

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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: March 11, 2006 08:27:10 ; Search time 349 Seconds  
(without alignments)

714.006 Million cell updates/sec

Title: US-09-541-462B-2

Perfect score: 616

Sequence: 1 MAAMDVDTPSGTNSGAGKK.....KTRQVCPLDNREWEFQKYGH 108

Scoring table: BL0SUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 7673375 seqs, 115346444 residues

Total number of hits satisfying chosen parameters: 15346750

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-MOPSL=frame_plus_p2n model -DEV=r1h
-Q=/abs/ABSSWBB_spool1/US09541462/runat_10032006_080737_22172/app_query.fasta_1
-DB=Published Applications NA_New -QFMT=FastA -SUFFIX=rnppn -MINMATCH=0.1
-LOOPCL=0 -LOOPBEXT=0 -UNITS=51s -START=1 -END=-1 -MATRIX=0|sum62
-TRANS=HOMO-CDI -LIS1=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFILE=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -HOSTSCORER=50h
-USER=US0951432@CGN_1_1_431@runat_10032006_080737_22172 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=10 -TREADES=1 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database :

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Published Applications NA_New:*
1: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq:*
2: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
3: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq:*
4: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq:*
5: /cgn2_6/prodata/2/pubpna/US05_NEW_PUB.seq:*
6: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq:*
7: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
8: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq:*
9: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
10: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
11: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
12: /cgn2_6/prodata/2/pubpna/US11_NEW_PUB.seq:*
13: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	527	85.6	660	9	US-11-096-568A-11809	Sequence 11809, A
2	516.5	83.8	432	9	US-11-096-568A-14405	Sequence 14405, A
3	515.5	83.7	693	9	US-11-096-568A-26820	Sequence 26820, A
4	499	81.0	348	9	US-11-096-568A-28569	Sequence 28569, A

## ALIGNMENTS

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RESULT 1
US-11-096-568A-11809
; Sequence 11809, Application US/11096568A
; Publication No. US20060048240A1
; GENERAL INFORMATION:
; APPLICANT: Alexandrov, Nickolai et al.
; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
; TITLE OF INVENTION: Theory
; FILE REFERENCE: 2750-1592PUS2
; CURRENT APPLICATION NUMBER: US/11/096_568A
; CURRENT FILING DATE: 2005-04-01
; NUMBER OF SEQ ID NOS: 34471
; SEQ ID NO 11809
; LENGTH: 660
; TYPE: DNA
; ORGANISM: Triticum aestivum
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (1) (660)
; OTHER INFORMATION: Ceres Seq. ID no. 11657464
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Alignment Scores:
Pred. No.: 1.97e-49
Score: 527.00
Percent Similarity: 79.8%
Best Local Similarity: 75.8%
Query Match: 85.6%
Length: 660
Matches: 94
Conservative: 5
Mismatches: 7
Indels: 18
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DB: 9 Gaps: 2

US-09-541-462B-2 (1-108) × US-11-096-568A-11809 (1-660)

QY 3 AlaAlaMetAspValAspThrProSer -----GlyThr 13

Db 88 TCGGCCATGAGACGGAGCAGCCCGAGGCCGCCCCGCGCC 147

QY 14 AsnSerGlyAlaGlyLys-----LysArgPheGluVal 24

Db 148 GACGCCGGCCGGCTCTGGCTCTCGCAAGGGCAAGGGCTCGAGATC 207

QY 25 LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspLysValAsnCysAlaLe 44

Db 208 AAGAGTGGAAAGCGGTCGGCTGGGACATCTGGGACACTGGCAC 267

QY 45 CysAlaGlyHisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThr 64

Db 268 TGCCCTAACCATCATGGATTATGCAATGAGTCGCCAAACGGCCAGGCCACC 327

QY 65 SerGluGluCysThrValAlaTrpGlyValCysAlaPheHisPheHisCysIle 84

Db 328 AGCGGAGTGACCGTCGATGGGTGTCGATCTCCATGCTTCAC 387

QY 85 SerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGln 104

Db 388 AGCACTGGCTCAAATCTGCAACTAGACAGGAATGGAGTCAG 447

QY 105 LysTrpGlyHis 108

Db 448 AAATAGGCCAC 459

RESULT 2

US-11-096-568A-14405

Sequence 14405, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TYPE: DNA

FEATURE: misc\_feature

NAME/KEY: misc\_feature

LOCATION: (1) .(432)

OTHER INFORMATION: Ceres Seq. ID no. 4776740

US-11-096-568A-14405

OTHER INFORMATION: Ceres Seq. ID no. 4776740

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO: 14405

LENGTH: 432

TYPE: DNA

FEATURE: misc\_feature

NAME/KEY: misc\_feature

LOCATION: (1) .(432)

OTHER INFORMATION: Ceres Seq. ID no. 4776740

US-09-541-462B-2 (1-108) × US-11-096-568A-26820 (1-633)

QY 52 LeucysIleGluCysGlnAlaAsnGlnAlaSerGluGluCysThrValAla 71

Db 257 CTCGTATGAACTCAGGCTTAATCAGGCCCTACGAGTGGGAATGCACTTGCT 316

QY 72 TrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArg 91

Db 317 TGGGGTTGCAATCACCCCTCACTTCAGCTACAGTGGATGGTTAACACTCGT 376

QY 92 GluValCysProLeuAspAsnArgGluTrpGluPheGlnLysTrpGlyHis 108

Db 377 CAACTTGCCATTGATAAACAGTGAATGGAGTTCAGAAATAATGGTCAC 427

RESULT 3

US-11-096-568A-26820

Sequence 26820, Application US/11096568A

Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides

TYPE: DNA

FEATURE: misc\_feature

NAME/KEY: misc\_feature

LOCATION: (1) .(693)

OTHER INFORMATION: Ceres Seq. ID no. 13622871

US-11-096-568A-26820

Alignment Scores:

Pred. No.: 4\_056-48

Score: 515.50

Percent Similarity: 87.3%

Best Local Similarity: 83.6%

Query Match: 83.7%

DB: 9

Length: 693

Matches: 92

Mismatches: 9

Indels: 5

Gaps: 2

US-09-541-462B-2 (1-108) × US-11-096-568A-26820 (1-633)

QY 4 AlaMetAsp-----ValAspThrProSerGlyThrAsnSerGlyAlaGlyLys--- 693

Db 108 GCGATGCCAACGGCAGCGTCGTGCGCCCTGCGGCCCTGGGACATCGAAAG 167

QY 20 --LysArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleVal 38

Db 168 GCGAAGGGCTTCGAGATCAAGAAGTGAACGCCCTCCTCTGGGACATCGTG 227

QY 39 ValAspAsnCysAlaLysCysArgAsnHistLeuAspIleGluCysGlnAla 58

Db 228 GTGGAAACTCGGCCATCAGGCCAACCATCATGACCTTGCATCGAGTGGCAGGG 287

QY 59 AsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAla 78

Db 288 AACACGGGACGCCACGGAGATGCGCTGGAAAGGCCCTCTGGGAAATTGAAACCATGCA 347

QY 79 PheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsn 98

Db 348 TTCACTTCACTGATCAAGCTGCTGGCTAAAGGCCGTCAGTGTGCCCCTCTGTGAAAC 407

QY 99 ArgGluTrpGluPheGlnLysTrpGlyHis 108

Db 408 AGTGAATGGAGTCCAGAAAGTGTGAACTGGTAC 437

RESULT 4

US-11-096-568A-28569

Sequence 28569, Application US/11096568A  
 Publication No. US20060048240A1

GENERAL INFORMATION:

APPLICANT: Alexandrov, Nickolai et al.

TITLE OF INVENTION: Therby

FILE REFERENCE: 2750-1592PUS2

CURRENT APPLICATION NUMBER: US/11/096, 568A

CURRENT FILING DATE: 2005-04-01

NUMBER OF SEQ ID NOS: 34471

SEQ ID NO: 28569

LENGTH: 348

TYPE: DNA

ORGANISM: Arabidopsis thaliana  
 FEATURE:

LOCATION: (1) .(348)

OTHER INFORMATION: Ceres Seq. ID no. 3017472

US-11-096-568A-28569

Alignment Scores:

Pred. No.: 1.27e-6

Score: 499.00

Percent Similarity: 86.1%

Best Local Similarity: 81.5%

Query Match: 81.0%

DB: 9

US-09-541-462B-2 (1-108) × US-11-096-568A-28569 (1-348)

Qy 1 MetAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20

Db 28 ATGGGTAAATCCCTCATCTCCGPACCTTC-----TCCTCGCAGAACCTCGAAA 81

Qy 21 ArgPheIuvalLysSrtPAsnAlaValAlaLeuTerPalaTrPaspIleValAsp 40

Db 82 CGATTTCAATTAAAGAAGTGTGAAGTGTCTCTCTGGGTTGGGATATCGTTCTTGAT 141

Qy 41 AsnCysBalalleCysArgAsnHisIleMetAspLeuCysIleGlucysGlnAlaAsnGln 60

Db 142 AACTGCCAATTGTAGGAATCACATGATCTCTGTATTGATGCTAGCTPATCAA 201

Qy 61 AlaSerAlaThrSerGluGlucysThrValAlaTrPgyValCysAsnHisAlaPheHis 80

Db 202 GCTAGTCCCACTAGTGGGAATGCACTGTTGCTGCTGGGTTGCNAACCAGCCTTAC 261

Qy 81 PheHisCysSleSerArgTrPleuLysThrArgGlnValCysProLeuAspAsnArgGlu 100

Db 262 TTCCCACTGTATCAGCAGATGGCTCAAAACTCGTCAGGTGTTCCACTAGTGTCTGCGAG 321

Qy 101 TrpGluTheGinLyStyrglyHis 108

Db 322 TGGGAATTCAGAAATATGGTCAC 345

RESULT 5

Publication No. US/10932182A

GENERAL INFORMATION:

APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHIRO

APPLICANT: KODAMA, YUKIKO

APPLICANT: FUJIMURA, TOMOKO

APPLICANT: ASHIKARI, TOSHIHIKO

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: 030685-043

CURRENT APPLICATION NUMBER: US/10/932, 182A

CURRENT FILING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 19703

SOFTWARE: PatentIn version 3.3

LENGTH: 366

TYPE: DNA

ORGANISM: Saccharomyces pastorianus

US-10-932-182A-78459

Sequence 78459, Application US/10932182A

GENERAL INFORMATION:

APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHIRO

APPLICANT: KODAMA, YUKIKO

APPLICANT: FUJIMURA, TOMOKO

APPLICANT: ASHIKARI, TOSHIHIKO

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: 030685-043

CURRENT APPLICATION NUMBER: US/10/932, 182A

CURRENT FILING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 19703

SOFTWARE: PatentIn version 3.3

LENGTH: 366

TYPE: DNA

ORGANISM: Saccharomyces pastorianus

US-10-932-182A-78459

Sequence 78459, Application US/10932182A

GENERAL INFORMATION:

APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHIRO

APPLICANT: KODAMA, YUKIKO

APPLICANT: FUJIMURA, TOMOKO

APPLICANT: ASHIKARI, TOSHIHIKO

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: 030685-043

CURRENT APPLICATION NUMBER: US/10/932, 182A

CURRENT FILING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 19703

SOFTWARE: PatentIn version 3.3

LENGTH: 366

TYPE: DNA

RESULT 6

US-10-932-182A-78459

Sequence 78459, Application US/10932182A

GENERAL INFORMATION:

APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHIRO

APPLICANT: KODAMA, YUKIKO

APPLICANT: FUJIMURA, TOMOKO

APPLICANT: ASHIKARI, TOSHIHIKO

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: 030685-043

CURRENT APPLICATION NUMBER: US/10/932, 182A

CURRENT FILING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 19703

SOFTWARE: PatentIn version 3.3

LENGTH: 366

TYPE: DNA

ORGANISM: Saccharomyces pastorianus

US-10-932-182A-78459

Sequence 78459, Application US/10932182A

GENERAL INFORMATION:

APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHIRO

APPLICANT: KODAMA, YUKIKO

APPLICANT: FUJIMURA, TOMOKO

APPLICANT: ASHIKARI, TOSHIHIKO

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: 030685-043

CURRENT APPLICATION NUMBER: US/10/932, 182A

CURRENT FILING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 19703

SOFTWARE: PatentIn version 3.3

LENGTH: 366

TYPE: DNA

ORGANISM: Saccharomyces pastorianus

US-10-932-182A-78459

Sequence 78459, Application US/10932182A

GENERAL INFORMATION:

APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHIRO

APPLICANT: KODAMA, YUKIKO

APPLICANT: FUJIMURA, TOMOKO

APPLICANT: ASHIKARI, TOSHIHIKO

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: 030685-043

CURRENT APPLICATION NUMBER: US/10/932, 182A

CURRENT FILING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 19703

SOFTWARE: PatentIn version 3.3

LENGTH: 366

TYPE: DNA

ORGANISM: Saccharomyces pastorianus

US-10-932-182A-78459

Sequence 78459, Application US/10932182A

GENERAL INFORMATION:

APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHIRO

APPLICANT: KODAMA, YUKIKO

APPLICANT: FUJIMURA, TOMOKO

APPLICANT: ASHIKARI, TOSHIHIKO

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: 030685-043

CURRENT APPLICATION NUMBER: US/10/932, 182A

CURRENT FILING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 19703

SOFTWARE: PatentIn version 3.3

LENGTH: 366

TYPE: DNA

ORGANISM: Saccharomyces pastorianus

US-10-932-182A-78459

Sequence 78459, Application US/10932182A

GENERAL INFORMATION:

APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHIRO

APPLICANT: KODAMA, YUKIKO

APPLICANT: FUJIMURA, TOMOKO

APPLICANT: ASHIKARI, TOSHIHIKO

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: 030685-043

CURRENT APPLICATION NUMBER: US/10/932, 182A

CURRENT FILING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 19703

SOFTWARE: PatentIn version 3.3

LENGTH: 366

TYPE: DNA

ORGANISM: Saccharomyces pastorianus

US-10-932-182A-78459

Sequence 78459, Application US/10932182A

GENERAL INFORMATION:

APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHIRO

APPLICANT: KODAMA, YUKIKO

APPLICANT: FUJIMURA, TOMOKO

APPLICANT: ASHIKARI, TOSHIHIKO

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: 030685-043

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APPLICANT: FUJIMURA, TOMOKO

APPLICANT: ASHIKARI, TOSHIHIKO

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FILE REFERENCE: 030685-043

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NUMBER OF SEQ ID NOS: 19703

SOFTWARE: PatentIn version 3.3

LENGTH: 366

TYPE: DNA

ORGANISM: Saccharomyces pastorianus

US-10-932-182A-78459

Sequence 78459, Application US/10932182A

GENERAL INFORMATION:

APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHIRO

APPLICANT: KODAMA, YUKIKO

APPLICANT: FUJIMURA, TOMOKO

APPLICANT: ASHIKARI, TOSHIHIKO

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

FILE REFERENCE: 030685-043

CURRENT APPLICATION NUMBER: US/10/932, 182A

CURRENT FILING DATE: 2004-09-02

NUMBER OF SEQ ID NOS: 19703

SOFTWARE: PatentIn version 3.3

LENGTH: 366

TYPE: DNA

ORGANISM: Saccharomyces pastorianus

US-10-932-182A-78459

Sequence 78459, Application US/10932182A

GENERAL INFORMATION:

APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHIRO

APPLICANT: KODAMA, YUKIKO

APPLICANT: FUJIMURA, TOMOKO

APPLICANT: ASHIKARI, TOSHIHIKO

TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

QY 19 -----LysLysArgPheGluValLysTrpAsnAlaValAlaLeuTrpAla 34  
 DB 82 GTGGAAACAAAAGAAGATGAAATTAGAATGTTGAACTGGTTCGTC 141  
 QY 35 TrpAspIleValAspAsnCysAlaLleCysArgAsnHisIleMetAspLeuCyste 54  
 DB 142 TGGGATATACTGTGACAACTGTGCTATTGCAAGAACATAATGAAACCATT 201  
 QY 55 GluCysGlnAlaArgGlnAlaSerAlaThrSerGluGlyCysThrValAlaTrpGlyAla 74  
 DB 202 GAATGCCAGCAAAGCCATGACGGACACTGATAATGAACTGGCTGGTGC 261  
 QY 75 CysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCys 94  
 DB 262 TGTATCACCCCTTGCAATTGCACTTGATGAACTAGAGAGAGCGCTGC 321  
 QY 95 ProLeuAspAsnArgGluTrpGluPheGlnLysTrgI 107  
 DB 322 CCATTAGATAACCAACCTTGCACTTGCAAGTAGCATGCGGT 360

## RESULT 7

US-10-932-182A-2279  
 ; Sequence 2279, Application US/10932182A  
 ; Publication No. US 0000046253A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NAKAO, YOSHIHIRO  
 ; APPLICANT: NAKAMURA, NORIHIWA  
 ; APPLICANT: FUJIMURA, YUKIKO  
 ; APPLICANT: ASHIKARI, TOSHIHIKO  
 ; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
 ; FILE REFERENCE: 030685-043  
 ; CURRENT APPLICATION NUMBER: US/10/932,182A  
 ; CURRENT FILING DATE: 2004-09-02  
 ; NUMBER OF SEQ ID NOS: 197023  
 ; SEQ ID NO: 2279  
 ; LENGTH: 366  
 ; TYPE: DNA  
 ; ORGANISM: *Saccharomyces pastorianus*  
 US-10-932-182A-2279

Alignment Scores:  
 Pred. No.: 2.25e-33 Length: 366  
 Score: 381.00 Matches: 62  
 Percent Similarity: 73.0% Conservative: 11  
 Best Local Similarity: 62.0% Mismatches: 23  
 Query Match: 61.9% Indels: 4  
 DB: 73 AATTCACCGTAGGACCAA-----AAAAAGATTCGATTAAATCG 120

US-09-541-462B-2 (1-108) x US-10-932-182A-2279 (1-366)

QY 8 AspThrProSerGlyThrAsnSerGlyAlaGlyLysArgPheGluValLysTrp 27  
 DB 73 AATTCACCGTAGGACCAA-----AAAAAGATTCGATTAAATCG 120

QY 28 AsnAlaValAlaLeuTrpAlaTrpAspIleValAspAsnCysAlaLeuCysArgAsn 47  
 DB 121 ACACGGTGGCTCTGGATCATGAACTGGCTGGATATAGCCGTTGAGAAC 180

QY 48 HisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGlu 67  
 DB 181 CACATTATGAAACATGCAATGAACTGGCTGGATATAGCCGTTGAGAAC 240

QY 68 CysThrValAlaTrpGlyValCysAsnHiSalAlaPheHiSpheroHiCysIleSerArgTrp 87  
 DB 241 TGTTGGCCGCCATGGGTTGTTGAAATCAGCTTCCACTTGCACATGCACTGCACTTAATG 300

QY 88 LeuIleThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTrgI 107  
 DB 301 ATCAAGACGAGATGATGCCCTTGGCAACACTTGGCAAGGTGGCT 360

## RESULT 9

US-10-821-234-554  
 ; Sequence 554, Application US/10821234  
 ; Publication No. US 00050255114A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Label, Ivan  
 ; APPLICANT: Stache-Crain, Birgit  
 ; APPLICANT: Anarmani, Susan  
 ; APPLICANT: Tang, Y. Tom  
 ; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
 ; FILE REFERENCE: 821A  
 ; CURRENT APPLICATION NUMBER: US/10/821,234  
 ; CURRENT FILING DATE: 2004-04-07  
 ; PRIORITY APPLICATION NUMBER: US 60/462,047  
 ; PRIOR FILING DATE: 2003-04-07  
 ; NUMBER OF SEQ ID NOS: 1704  
 ; SOFTWARE: pt\_seq\_genes Version 1.0  
 ; SEQ ID NO: 554  
 ; LENGTH: 342  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-821-234-554

QY 8 AspThrProSerGlyThrAsnSerGlyAlaGlyLysArgPheGluValLysTrp 27  
 DB 73 AATACACGGTAGAGACAATA-----AAAAAGATTCGATTAAATCG 120

QY 28 AsnAlaValAlaLeuTrpAlaTrpAspIleValAsnCysAlaLeuCysArgAsn 47  
 DB 121 ACAGCGCTGGCGTCTGGATATAGCCGTTGACAATGTGCACATTGCAAAAC 180

QY 48 HisIleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaLeuAlaThrSerGluGlu 67  
 DB 181 CACATTATGAAACATGCAATGAACTGGCTGGATATAGCCGTTGAGAAC 240

QY 68 CysThrValAlaTrpGlyValCysAsnHiSalAlaPheHiSpheroHiCysIleSerArgTrp 87  
 DB 241 TGTTGGCCGCCATGGGTTGTTGAAATCAGCTTCCACTTGCACATGCACTGCACTTAATG 300

QY 88 LeuIleThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTrgI 107  
 DB 301 ATCAAGACGAGATGATGCCCTTGGCAACACTTGGCAAGGTGGCT 360

## RESULT 8





APPLICANT: Edwards, Jean-Baptiste Dumas Milne  
 i APPLICANT: Ducleit, Aymeric  
 i APPLICANT: Bougnieret, Lydie  
 i APPLICANT: Jobert, Severin  
 i APPLICANT: Cluseel, Catherine  
 i TITLE OF INVENTION: Complementary DNA's Encoding Proteins with Signal Peptides  
 i FILE REFERENCE: 56.USA.CIP  
 CURRENT APPLICATION NUMBER: US/09/978,360A  
 CURRENT FILING DATE: 2001-10-15  
 i PRIOR APPLICATION NUMBER: US 60/066,677  
 PRIOR FILING DATE: 1997-11-13  
 i PRIOR APPLICATION NUMBER: US 60/069,957  
 PRIOR FILING DATE: 1997-12-17  
 i PRIOR APPLICATION NUMBER: US 60/074,121  
 PRIOR FILING DATE: 1998-02-09  
 i PRIOR APPLICATION NUMBER: US 60/081,563  
 PRIOR FILING DATE: 1998-04-13  
 i PRIOR APPLICATION NUMBER: US 60/096,116  
 PRIOR FILING DATE: 1998-08-10  
 i PRIOR APPLICATION NUMBER: US 60/099,273  
 PRIOR FILING DATE: -09-04  
 i PRIOR APPLICATION NUMBER: US 09/191,997  
 PRIOR FILING DATE: 1998-11-13  
 i PRIOR APPLICATION NUMBER: US 09/215,435  
 PRIOR FILING DATE: 1998-12-17  
 i PRIOR APPLICATION NUMBER: PCT/IB98/02122  
 PRIOR FILING DATE: 1998-12-17  
 i PRIOR APPLICATION NUMBER: US 09/247,155  
 PRIOR FILING DATE: 1999-02-09  
 Remaining Prior Application data removed - See File Wrapper or PALM.  
 SOFTWARE: Patent.pml  
 SEQ ID NO: 810  
 LENGTH: 648  
 TYPE: DNA  
 ORGANISM: Homo Sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 187..438  
 FEATURE:  
 NAME/KEY: polyA\_signal  
 LOCATION: 612..617  
 FEATURE:  
 NAME/KEY: polyA\_site  
 LOCATION: 632..648  
 US-09-978-360A-4  
 Alignment Scores:  
 Pred. No.: 1.06e-14 Length: 648  
 Score: 217.00 Matches: 43  
 Percent Similarity: 44.5% Conservative: 18  
 Best Local Similarity: 31.4% Mismatches: 40  
 Query Match: 35.2% Indels: 3  
 DB: 5  
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 QY 2 AlaAlaAlaLysAspValApThrProSerGlyLysLysArg 21  
 DB 49 GCGGCACTGIGGTCATTATACCTTCCGGGACTGCAAACGGAAGC 108  
 QY 22 PheGlu------23  
 DB 109 GCGGACGGAGGTCTGCTGCATGTTGGCATTCGGGACTG 168  
 QY 24 -----33  
 DB 169 ACGTGAGGCTCTGGCAACATGAGTAAAGTGTGGCAACCTG 228  
 QY 34 AlaTPAspIleValValApAsnCysAlaIleCysArgAsnHisIleMetAspLeuCys 53  
 DB 229 CTCCTGGCAACATGAGAActCTGGCATCTCAGGATTAACGGATGTGCC 288

Qy 54 IleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrValAlaTrpGly 73  
 Db 289 CCTGACTGCAG-----GTCGGCGGACACTGCCGCTGTCGGGGC 333

Qy 74 ValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnVal 93  
 Db 334 CAGTGTCCCAACTGCTTCCACATGATTGATCTCAAGTGGCTCACGCACAGGGTG 393

Qy 94 -----CysProLeuAspAsnArgGluTrpGluPheGlnLysTyrgly 107  
 Db 394 CAGCAGCACTGCCCATGTCGGAGATGGAAAGTCAAGGAGTGGCC 444

RESULT 15  
 US-11-057-484A-14  
 Sequence 14, Application US/11057484A  
 i GENERAL INFORMATION:  
 i PUBLICATION NO. US20060029331A1  
 i APPLICANT: Finke, Terri H.  
 i APPLICANT: Yin, Jiyi  
 i TITLE OF INVENTION: Cellular Genes Regulated by HIV-1  
 i TITLE OF INVENTION: Infection and Methods of Use Thereof  
 i FILE REFERENCE: CHOP\_0146CIP  
 i CURRENT APPLICATION NUMBER: US/11/057,484A  
 i CURRENT FILING DATE: 2005-02-14  
 i PRIOR APPLICATION NUMBER: US 10/368,803  
 i PRIOR FILING DATE: 2003-02-19  
 i PRIOR APPLICATION NUMBER: US 60/358,495  
 i PRIOR FILING DATE: 2002-02-19  
 i NUMBER OF SEQ ID NOS: 25  
 i SOFTWARE: FastSEQ for Windows Version 3.0  
 i SEQ ID NO: 14  
 i LENGTH: 450  
 i TYPE: DNA  
 i ORGANISM: Homo sapien  
 i FEATURE:  
 i NAME/KEY: misc feature  
 i LOCATION: (0)..(0)  
 i OTHER INFORMATION: n = A, C, G or T  
 US-11-057-484A-14

Alignment Scores:  
 Pred. No.: 1.15e-14 Length: 450  
 Score: 215.00 Matches: 41  
 Percent Similarity: 53.6% Conservative: 11  
 Best Local Similarity: 42.3% Mismatches: 23  
 Query Match: 34.9% Indels: 23  
 DB: 9 Gaps: 2

US-09-541-462B-2 (1-108) x US-11-057-484A-14 (1-450)  
 Qy 11 SerGlyThrAsnSerGlyAlaGlyLysLysArgTheGluValBtysLysTrpAspAlaVal 30  
 Db 54 TCAGGCTCCAAGTGGGA--GGGACAAGATGTTCTCCCTCAAGAAGTGGAAACGGGTG 110  
 Qy 31 AlaLeuTrpAlaLysAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMet 50  
 Db 111 GCCTGTGAGTCGAGCTGGAGTCGCTACGGCCATCTCAGGT-----160

Qy 71 AlaTrpGlyValCysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuYsthr 90  
 Db 167 GTCTGGGAGAATTAACATTCCTCCAACTGATGTCCTGTTGGAAACAG 226

Qy 51 AspIleCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70  
 Db 161 -----

Qy 91 ArgGlnValCysProLeuAspAsnArgGluTrpGluPheGlnLysTyrgly 107  
 Db 227 AACATGNTGCCTCTCGCCACAGCTGGTCAAAATACTGG 277



9

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OM protein - nucleic search, using frame\_plus\_P2n model

Run on: March 11, 2006, 08:13:49 ; Search time 134 Seconds  
(without alignments)

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Title: US-09-541-462B-2

Perfect score: 616

Sequence: 1 MAAMDVDTPSCTNSGAGK.....KTRQVCPLDNREWFKYGH 108

Scoring table: BLASTM62

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delect 7.0

Searched: 1303057 seqs, 888780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

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-LOOPEXT=0 -DOUALIGN=200 -START=1 -END=1 -MATRIX=blosum62 -TRANS=human10.cdi
-LIST=45 -TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-MODE=LOCAL -OUTFMT=pio -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=USER=US9541462 @runat_10032006_080729_220008
-NCPU=6 -ICPU=3 -NO NMMP -NEG SCORES=0 -WAIT =DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXTH=7
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- 2: /cgn2\_6/ptcdatal1/in1/in5\_comb.seq:\*
- 3: /cgn2\_6/ptcdatal1/in1/6A\_comb.seq:\*
- 4: /cgn2\_6/ptcdatal1/in1/6B\_comb.seq:\*
- 5: /cgn2\_6/ptcdatal1/in1/H\_comb.seq:\*
- 6: /cgn2\_6/ptcdatal1/in1/PCUTS\_comb.seq:\*
- 7: /cgn2\_6/ptcdatal1/in1/PP\_comb.seq:\*
- 8: /cgn2\_6/ptcdatal1/in1/RE\_comb.seq:\*
- 9: /cgn2\_6/ptcdatal1/in1/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

**SUMMARIES**

Result No.	Score	Query	Match	Length	DB ID	Description
1	616	100.0	482	3	US-09-513-999C-3894	Sequence 3894, Ap
2	616	100.0	504	3	US-09-944-322A-5	Sequence 5, Appli
3	616	100.0	507	3	US-09-949-0324A-3	Sequence 4940, Ap
4	616	100.0	508	3	US-09-914-322A-3	Sequence 3, Appli
5	501.5	81.4	3208	3	US-09-780-016-27	Sequence 27, Appli
6	501.5	81.4	3208	3	US-10-214-811-27	Sequence 27, Appli
7	501.5	81.4	3208	3	US-10-766-074-27	Sequence 1731, Appli
8	400.5	77.8	411	3	US-09-440-211A-1731	Sequence 26812, A
c	400.5	65.0	1101	3	US-09-270-767-11265	Sequence 11265, A
c	11	394	64.0	402	US-09-513-999C-10371	Sequence 10371, A
c	12	394	64.0	463	US-09-621-970-15180	Sequence 4, Appli
c	13	385	62.5	480	US-09-914-324A-4	Sequence 5495, Ap
c	14	375.5	61.0	357	US-09-248-796-5195	Sequence 7, Appli
c	15	287	46.6	342	US-09-846-312A-7	Sequence 7, Appli
c	16	287	46.6	342	US-09-942-497A-7	Sequence 7, Appli
c	17	287	46.6	342	US-10-108-767-7	Sequence 492, App
c	18	262.5	42.6	301	US-09-313-29A-492	Sequence 27, Appli
c	19	217	35.2	648	US-09-539-360B-27	Sequence 1817, Ap
c	20	200.5	32.5	534	US-09-621-976-181	Sequence 1854, Ap
c	21	198	32.1	671	US-09-621-976-1854	Sequence 2051, Ap
c	22	197.5	32.1	539	US-09-521-976-2051	Sequence 1945, Ap
c	23	191	31.0	654	US-09-621-976-1945	Sequence 16682, A
c	24	175	28.4	25274	US-09-949-016-16662	Sequence 10, Appli
c	25	173	28.1	585	US-09-270-767-10788	Sequence 10788, A
c	26	150.5	24.4	439	US-09-799-451-296	Sequence 296, App
c	27	146	23.7	170	US-09-270-767-26553	Sequence 26253, A
c	28	137.5	22.3	2135	US-10-104-047-459	Sequence 459, App
c	29	91	14.8	940	US-09-923-655-667	Sequence 667, App
c	30	91	14.8	1839	US-09-938-303-10	Sequence 10, App
c	31	90	14.6	872	US-09-774-528-304	Sequence 304, App
c	32	90	14.6	872	US-10-120-988-304	Sequence 304, App
c	33	90	14.6	893	US-09-949-016-4980	Sequence 4980, Ap
c	34	90	14.6	1690	US-09-928-303-2	Sequence 2, Appli
c	35	90	14.6	3140	US-10-120-988-255	Sequence 255, App
c	36	90	14.6	3140	US-10-120-988-255	Sequence 255, App
c	37	90	14.6	8438	US-07-945-283-1	Sequence 1, Appli
c	38	88	14.3	1183	US-09-799-431-763	Sequence 763, Ap
c	39	88	14.3	1976	US-10-104-047-17680	Sequence 1680, Ap
c	40	86	14.0	363	US-09-640-211A-1119	Sequence 1319, Ap
c	41	86	14.0	1267	US-09-949-016-378	Sequence 378, Ap
c	42	86	14.0	1267	US-09-949-016-2914	Sequence 2914, Ap
c	43	85.5	13.9	3304	US-09-799-431-220	Sequence 220, Ap
c	44	85	13.8	1621	US-09-923-655-20	Sequence 20, Appli
c	45	85	13.8	1995	US-09-949-016-3134	Sequence 3134, Ap

**ALIGNMENTS**

RESULT 1  
US-09-513-999C-3894  
Sequence 3894, Application US/09513999C

GENERAL INFORMATION:  
 / APPLICANT: Dumas Milne Edwards, J.B.  
 / ATTORNEY: Ducleart, A.  
 / APPLICANT: Giordano, J.Y.  
 / TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
 / Patent No. 6783961  
 / FILE REFERENCE: 59.US2.REG  
 / CURRENT APPLICATION NUMBER: US/09-513-999C  
 / FILING DATE: 2000-02-24  
 / PRIOR APPLICATION NUMBER: US 60/1122,487  
 / PRIORITY FILING DATE: 1999-02-26  
 / NUMBER OF SEQ ID NOS: 36681  
 / SOFTWARE: Patent, pm  
 / SEQ ID NO: 3894  
 / LENGTH: 482  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / FEATURE: CDS  
 / LOCATION: 29..352  
 / FEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 401  
 / OTHER INFORMATION: r-a or g  
 / PEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 404  
 / OTHER INFORMATION: m-a or g  
 / PEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 26812  
 / OTHER INFORMATION: m-a or c  
 / PEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 378  
 / OTHER INFORMATION: m-a or c  
 / PEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 304  
 / OTHER INFORMATION: m-a or c  
 / PEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 255  
 / OTHER INFORMATION: r-a or g  
 / PEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 220  
 / OTHER INFORMATION: m-a or c  
 / PEATURE:  
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 / LOCATION: 2051  
 / OTHER INFORMATION: m-a or c  
 / PEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 1319  
 / OTHER INFORMATION: m-a or c  
 / PEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 10788  
 / OTHER INFORMATION: m-a or c  
 / PEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 1817  
 / OTHER INFORMATION: m-a or c  
 / PEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 1680  
 / OTHER INFORMATION: m-a or c  
 / PEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 1334  
 / OTHER INFORMATION: m-a or c  
 / PEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 104  
 / OTHER INFORMATION: m-a or c  
 / PEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 940  
 / OTHER INFORMATION: m-a or c  
 / PEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 763  
 / OTHER INFORMATION: m-a or c  
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 / NAME/KEY: misc\_feature  
 / LOCATION: 667  
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 / NAME/KEY: misc\_feature  
 / LOCATION: 2914  
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 / PEATURE:  
 / NAME/KEY: misc\_feature  
 / LOCATION: 220  
 / OTHER INFORMATION: m-a or c  
 / PEATURE:  
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 / LOCATION: 168  
 / OTHER INFORMATION: m-a or c  
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 / NAME/KEY: misc\_feature  
 / LOCATION: 940  
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 / NAME/KEY: misc\_feature  
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 / NAME/KEY: misc\_feature  
 / LOCATION: 667  
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 / NAME/KEY: misc\_feature  
 / LOCATION: 2914  
 / OTHER INFORMATION: m-a or c  
 / PEATURE:  
 / NAME/KEY: misc\_feature  
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 Score: 616.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 3 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-513-99C-3894 (1-482)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyAlaGlyLysIys 20  
 Db 29 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAspIleValValAsp 40  
 Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAspIleValValAsp 40  
 Db 89 CGCTTGAAGTGAAATGGTAATGGATATTGGTTGAT 148

Qy 41 AsnCysAlaLalleCysArgArgAsnHistoleMetAspIleCysGlnAlaAsnGin 60  
 Db 149 AACCTGTCCATCTGAGAACCCATTTGATCATGAGCTAACGAGAAC 208

Qy 61 AlaseAlaThrSerGlyArgAsnHistoleMetAspIleCysGlnAlaAsnGin 60  
 Db 209 GCGTCGGCTACTCTGAAGGTGTACTGCTGGAGCTGGCTGTAAACATGCTTTCA 268

Qy 81 PheHisCysteSerArgTrpLeuIysThrArgGlnValCysProLeuAspAspArgGlu 100  
 Db 269 TTCCACTGCACTCTGCTGTCAGCATTTGATCATGAGCTAACGAGAAC 328

Qy 101 TrpGluPheGlnLysTrpGlyHis 108  
 Db 329 TGGGAATCCAAAAGTAGTGGCAC 352

RESULT 2  
 US-09-914-324A-5 Sequence 5, Application US/0914324A  
 ; Patent No. 688709  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conway, Joan A.  
 ; APPLICANT: Conway, Ronald C.  
 ; APPLICANT: Kamura, Takumi  
 ; APPLICANT: Oklahoma Medical Research Foundation  
 ; TITLE OF INVENTION: No. 65587031 Component of von Hippel-Lindau Tumor Suppressor  
 ; FILE REFERENCE: 021044-004600US  
 ; CURRENT APPLICATION NUMBER: US/09/914,324A  
 ; PRIORITY FILING DATE: 2003-02-11  
 ; PRIORITY APPLICATION NUMBER: US 60/121,787  
 ; PRIORITY APPLICATION NUMBER: WO PCT/US00/04838  
 ; PRIOR FILING DATE: 2000-02-25  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 5  
 ; LENGTH: 504  
 ; TYPE: DNA  
 ; ORGANISM: Mus sp.  
 ; FEATURE: CDS  
 ; NAME/KEY: CDS  
 ; LOCATION: (18)..(344)  
 ; OTHER INFORMATION: Rbx1  
 ; US-09-914-324A-5

Alignment Scores:  
 Pred. No.: 1.57e-66 Length: 504  
 Score: 616.00 Matches: 108  
 Percent Similarity: 100.0% Mismatches: 0  
 Best Local Similarity: 100.0% Indels: 0  
 Query Match: 100.0% Gaps: 0

US-09-541-462B-2 (1-108) x US-09-949-016-4940 (1-507)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyAlaGlyLysIys 20  
 Db 7 ATGGCGACGGATGGATCTGCCGACCAACGGCGGGAGAG 66

Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAspIleValValAsp 40  
 Db 67 CGCTTGAAGTGAAATGGCAATGCACTGAGCCCTCTGSCCTGGATATTGGCTGTAT 126

Qy 41 AsnCysAlaLalleCysArgAsnHistoleMetAspIleGluCysGlnAlaAsnGin 60  
 Db 127 AACCTGTCCATCTGAGAACCAATTATGGATCTTGATAGGATCTTCAC 186

US-09-541-462B-2 (1-108) x US-09-914-324A-5 (1-504)

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyAlaGlyLysIys 20  
 Score: 616.00 Matches: 108  
 Percent Similarity: 100.0% Mismatches: 0  
 Best Local Similarity: 100.0% Indels: 0  
 Query Match: 100.0% Gaps: 0

Db 18 ATGGCGACGGATGGATCTGCCGACCAACGGCGGGAGAG 66

Qy 21 ArgPheGluValLysLysTrpAsnAlaValAlaLeuTrpAspIleValValAsp 40  
 Db 78 CGCTTGAAGTGAAATGGCAATGCACTGAGCCCTCTGSCCTGGATATTGGCTGTAT 137

Qy 41 AsnCysAlaLalleCysArgAsnHistoleMetAspIleCysIleGluCysGlnAlaAsnGin 60  
 Db 138 AACCTGTCCATCTGAGAACCAATTATGGATCTTCAC 197

Qy 61 AlaseAlaThrSerGlyArgAsnHistoleMetAspIleCysGlnAlaAsnGin 80  
 Db 198 GCGTCAGCTACTTCGAGAGTGTACGGTTCAGCTGCAACCATGGTCTTCAT 257

Qy 81 PheHisCysLysSerArgTrpLeuIysThrArgGlnValCysProLeuAspAspArgGlu 100  
 Db 258 TTCCACTGATCTCTGATGGCTCAANACGAGCAAGGTGTCTGGTSGACACAGACAG 317

Qy 101 TrpGluPheGlnLysTrpGlyHis 108  
 Db 318 TGCGAGTTCAGAAGTATGGCAT 341

RESULT 3  
 US-09-914-324A-5 Sequence 5, Application US/0914324A  
 ; Patent No. 612339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; CURRENT APPLICATION NUMBER: US/09/949,016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIORITY NUMBER: 60/241,755  
 ; PRIORITY FILING DATE: 2000-10-20  
 ; PRIORITY APPLICATION NUMBER: 60/237,768  
 ; PRIORITY NUMBER: 60/231,498  
 ; PRIORITY FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FASTSEQ for Windows Version 4.0  
 ; SEQ ID NO 4940  
 ; LENGTH: 507  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-949-016-4940

Alignment Scores:  
 Pred. No.: 1.58e-66 Length: 507  
 Score: 616.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 3 Gaps: 0

Qy 61 AlaserAlaThrSerGluGlucysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80  
 Db 187 GCTCCCTACTAGAGTGACTGTCCATGGAGCTGTAAACATGCTTCAC 246

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 247 TTCCACTGCATCTCTGGTCATAAACACGACAGCTGTCATTGGACAACAGAG 306

Qy 101 TrpGluIleGlnLysTyrGlyHis 108  
 Db 307 TGGAAATTCCAAAAGTAGTGGCAC 330

RESULT 4  
 US-09-914-324A-3  
 Sequence 3, Application US/0914324A  
 Patent No. 688709  
 GENERAL INFORMATION:  
 APPLICANT: Conway, Joan A.  
 APPLICANT: Conway, Ronald C.  
 APPLICANT: Kamara, Takumi  
 APPLICANT: Oklahoma Medical Research Foundation  
 TITLE OF INVENTION: No. 6855709-1 Component of von Hippel-Lindau Tumor Suppressor  
 FILE REFERENCE: 021044-004600US  
 CURRENT FILING DATE: 2003-02-11  
 PRIOR APPLICATION NUMBER: US/09/914,324A  
 PRIOR FILING DATE: 1999-02-26  
 PRIOR APPLICATION NUMBER: WO PCT/US00/04838  
 PRIOR FILING DATE: 2000-02-25  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO 3  
 LENGTH: 508  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (7) ..(333)  
 OTHER INFORMATION: Rbx1  
 US-09-914-324A-3

Alignment Scores:  
 Pred. No.: 1.58e-66 Length: 508  
 Score: 616.00 Matches: 108  
 Percent Similarity: 100.0% Conservative: 0  
 Best Local Similarity: 100.0% Mismatches: 0  
 Query Match: 100.0% Indels: 0  
 DB: 3 0 Gaps: 0

US-09-541-462B-2 (1-108) x US-09-780-016-27 (1-3208)

Qy 16 GlyAlaGlyLysLysArgPheGluValLysLysTrpAsnAlaLeuTrpAlaTrp 35  
 Db 2752 GGACCATAAAAAAA-----AAAAAAATGAATGCAAGCCCCCTCGCCCTGG 2802

Qy 36 AspIleValValAspAsnCysAlaLysCysArgAsnHisIleMetAspLeuCysIleGlu 55  
 Db 2803 GATATTGTTGGATACTGTCCATCTGAGAACCATATTGATTTGGATAGAA 2862

Qy 56 CysGlnAlaAsnGlnAlaSerAlaThrSerGluCysThrValIleTrpGlyValCys 75  
 Db 2863 TGTCAGCTAACCGGCGTCGTACTCGAAAGTGFACTGTGCAATGGGGCTGT 2922

Qy 76 AsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCysPro 95  
 Db 2923 AACATGCTTTCTACTTCCACTGTGCTCGCTCAAACAGACGGTGTGCCA 2982

Qy 96 LeuAspAsnArgGluTrpGluPhgGlnLysTyrGlyHis 108  
 Db 2983 TTGGACAACAGAGGTGGAAATTCAAAGTATGGCAC 3021

RESULT 6  
 US-10-214-811-27  
 Sequence 2, Application US/10214811  
 Patent No. 674321  
 GENERAL INFORMATION:  
 APPLICANT: Donoho, Gregory  
 APPLICANT: Scoville, John  
 APPLICANT: Turner, C. Alexander Jr.  
 APPLICANT: Friedrich, Glenn  
 APPLICANT: Abuin, Alejandro  
 APPLICANT: Zambrowicz, Brian  
 APPLICANT: Sands, Arthur T.  
 TITLE OF INVENTION: No. 674321el Human Proteases and

Qy 1 MetAlaAlaAlaMetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLys 20  
 Db 7 ATGGCGCAGGATGATGTTGATACCCGACGACAAACAGGGGGCAAGAG 66

Qy 21 ArgPheGluValLysIleTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAsp 40  
 Db 67 CGCTTGAACTGAAAGTGAATCGATGCCCTGGGATATTGCGTTGAT 126

Qy 41 AsnCysSAlaIleCysArgAsnHisIleMetAspLeuCysteGluCysGlnAlaAsnGin 60  
 Db 127 AACTGTCGCAATCTGAGAACCATATTGATCTGGATAGATGTCAGTAACAG 186

Qy 61 AlaserAlaThrSerGluGluCysThrValAlaTrpGlyValCysAsnHisAlaPheHis 80  
 Db 187 GCGTCGCTACTTCAGAGTGACTGTGCGATGGACTCTGTAAACATGCTTCAC 246

Qy 81 PheHisCysIleSerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGlu 100  
 Db 247 TTCCACTGCATCTCTGGCTCAAACAGACAGGTGTCCATTGGACAACAGAG 306

Qy 101 TrpGluIleGlnLysTyrGlyHis 108

TITLE OF INVENTION: Polynucleotides Encoding the Same  
FILE REFERENCE: LEX-0132-USA  
CURRENT FILING DATE: US/10/214, 811  
PRIOR APPLICATION NUMBER: US/09/780, 016  
PRIOR FILING DATE: 2002-08-07  
PRIOR APPLICATION NUMBER: US/09/780, 016  
PRIOR FILING DATE: 2002-08-09  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 27  
LENGTH: 3208

TYPE: DNA  
ORGANISM: homo sapiens  
US-10-214-811-27

Alignment Scores:  
Pred. No.: 2.1e-51 Length: 3208  
Score: 501.50 Matches: 88  
Percent Similarity: 95.7% Conservative: 1  
Best Local Similarity: 94.6%  
Query Match: 81.4%  
DB: 3

US-09-541-462B-2 (1-108) x US-10-766-074-27 (1-3208)

Qy 16 GlyAlaGlyLysylArgPheGluValLysLystrpAsnAlaValAlaLeuTrpAlaTrp 35  
Db 2752 GGAGCATAAAAAAA----AAAAATGGATGCACTAGGCCCTCGGCCRG 2802

Qy 16 AspIleValValAspIleCysAlaIleCysA9AsnHisIleMetAspLeuCysIleIeu 55  
Db 2803 GATTTGTTGTCATACTGTGCATCGCATACTGCAACATPATGGAACTTGTGATGAA 2862

Qy 56 CysGlnAlaAsnGlnAlaserAlaThrSerGluGlucySthralrpGlyvalCys 75  
Db 2863 TGAAGCTAACGGCTCGGTACTCGAGTAGAGGTACTCAGAGGTACTCTGCAATGGGGTGTCTG 2922

Qy 76 AsnHisAlaPheHisPheHisCysIleSerArgTrpIleLysThrArgClnValCysPro 95  
Db 2923 AACATGCTTTCACTTCACCTCTCGTGGCTCAACAGCAGGGTGTCTG 2982

Qy 96 LeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108  
Db 2983 TTGGACACACGAGAGTGSGGAATTCCAAAGTAATGGC 3021

RESULT 8  
US-09-640-211A-1731  
; Sequence 1731, Application US/09640211A  
; GENERAL INFORMATION:  
; APPLICANT: Wood, Marion  
; PARENT NO. 6833346  
; FILE REFERENCE: 11000.1021CU  
; CURRENT FILING DATE: 2000-08-16  
; NUMBER OF SEQ ID NOS: 2368  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO: 1731  
; LENGTH: 411

Qy 56 CysGlnAlaAsnGlnAlaserAlaThrSerGluGluCysIleValCys 75  
Db 2863 TGTCAGCTAACGGCGTCCGACTCTGAAAGTGTACTCTGCTGGCAATGGCTCA 2922

Qy 76 AsnHisAlaPheHisPheHisCysIleSerArgTrpIleLysThrArgClnValCysPro 95  
Db 2923 AACATGCTTTCACTTCACCTCTCGTGGCTCAACAGCAGGGTGTCTG 2982

Qy 96 LeuAspAsnArgGluTrpGluPheGlnLysTyrGlyHis 108  
Db 2983 TTGGACACACGAGAGTGSGGAATTCCAAAGTAATGGC 3021

RESULT 7  
US-10-766-074-27  
; Sequence 27, Application US/10766074  
; GENERAL INFORMATION:  
; APPLICANT: Donoho, Gregory  
; APPLICANT: Scoville, John  
; APPLICANT: Turner, C. Alexander Jr.  
; APPLICANT: Friedrich, Glenn  
; APPLICANT: Abbin, Alejandro  
; APPLICANT: Zambro, Brian  
; APPLICANT: Sands, Arthur T.  
TITLE OF INVENTION: Human Proteases and  
FILE REFERENCE: LEX-0132-USA  
CURRENT FILING DATE: 2004-01-28  
PRIOR APPLICATION NUMBER: US/10/214, 811  
PRIOR FILING DATE: 2002-08-07  
PRIOR APPLICATION NUMBER: US/09/780, 016  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: US/10/766, 074  
PRIOR FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 27  
LENGTH: 3208

Alignment Scores:  
Pred. No.: 7.79e-50 Length: 411  
Score: 479.00 Matches: 90  
Percent Similarity: 85.0% Conservative: 6  
Best Local Similarity: 79.6%  
Query Match: 77.8%  
DB: 3

US-09-541-462B-2 (1-108) x US-09-640-211A-1731 (1-411)

Qy 3 AlaAlaMetAspValAsp-----ThrProSer-----GlyThrAsnSerClyAla 17  
Db 74 GCTCAACGACACAGATGATGATTCCGAGGGTTCCGTCAGCTCAAGGCC 133



```

; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: 20
; OTHER INFORMATION: k=g or t
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: 38
; OTHER INFORMATION: s=g or c
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: 79
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-10371

Alignment Scores:
Pred. No.: 2.05e-39 Length: 402
Score: 39.00 Matches: 76
Percent Similarity: 73.1% Conservative: 0
Best Local Similarity: 73.1%
Query Match: 64.0%
DB: 3 GAGATGGC-----102

Pred. No.: 2.05e-39 Length: 402
Score: 39.00 Matches: 76
Percent Similarity: 73.1% Conservative: 0
Best Local Similarity: 73.1%
Query Match: 64.0%
DB: 35 ATGCAATGCTGATACCCGAGGCCAACAGCGCNGCAAGAAGCCTTGAAGTG 94

US-09-541-462B-2 (1-108) x US-09-621-976-15180 (1-463)

Qy 5 MetAspValAspThrProSerGlyThrAsnSerGlyAlaGlyLysArgPheGluVal 24
Db 35 ATGCAATGCTGATACCCGAGGCCAACAGCGCNGCAAGAAGCCTTGAAGTG 94

Qy 25 LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAspAsnCysAlaIle 44
Db 95 AAAAGGC-----102

Qy 45 CyshArgAsnHistoleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThr 64
Db 103 - -----135

Qy 45 CyshArgAsnHistoleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThr 64
Db 103 - -----135

Qy 65 SerGluGluCysThrValAlaTrpGlyAlaGlyLysLysArgPheGluVal 24
Db 40 ATCGATGTGGATACCCGAGGCCAACAGCGCNGCAAGAAGGCTTTGAACTG 99

Qy 25 LysLysTrpAsnAlaValAlaLeuTrpAlaTrpAspIleValAspAsnCysAlaIle 44
Db 100 AAAAGGC-----107

Qy 45 CyshArgAsnHistoleMetAspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThr 64
Db 108 -----140

Qy 65 SerGluGluCysThrValAlaTrpGlyAlaGlyLysLysArgPheHisCyste 84
Db 141 TCAGAAGATGTACTGTCCTCATGGAGCTGTAAATGCTTCACTGCCACTGKTC 200

Qy 85 SerArgTrpLeuLysThrArgGlnValCysProLeuAspAsnArgGluTrpGluPheGln 104
Db 201 TCTCGCTGCCTCAAACGACAGCTGCTCCATTGGACAACAGAACGACTGGAAATCTCAA 260

Qy 105 LysTrpGlyHis 108
Db 261 AAGATGGCAC 272

RESULT 13
US-09-914-324A-4
; Sequence 4, Application US/09914324A
; Patent No. 6858709
; GENERAL INFORMATION:
; APPLICANT: Conway, Joan A.
; APPLICANT: Conway, Ronald C.
; APPLICANT: Kamura, Takumi
; APPLICANT: Oklamoma Medical Research Foundation
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; TITLE OF INVENTION: Complex and SCF Ubiquitin Ligase
; CURRENT APPLICATION NUMBER: US/09/914,324A
; FILE REFERENCE: 1044-00460US
; CURRENT FILING DATE: 2003-02-11
; PRIORITY NUMBER: US 60/121,787
; PRIORITY NUMBER: 1999-02-26
; PRIORITY NUMBER: WO PCT/US00/04838
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 4
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4)..(369)
; OTHER INFORMATION: Rbx1
US-09-914-324A-4

Alignment Scores:
Pred. No.: 3.3e-38 Length: 480
Score: 385.00 Matches: 64
Percent Similarity: 65.5%
Best Local Similarity: 56.6%
Mismatches: 29
Indels: 1
Query Match: 62.5%
DB: 3

US-09-541-462B-2 (1-108) x US-09-914-324A-4 (1-480)

; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: 15180, Application US/09621976
; GENERAL INFORMATION:
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
SEQ ID NO 15180
LENGTH: 463
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: 74
OTHER INFORMATION: n=a, g, c or t
US-09-621-976-15180

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5 MetAspPvalAspThrProSerGlyThrAsnSerGlyAlaGly----- 18  
 25 ATGGATGTGATGAAGTGAATCGCAAATAATTGGCAAAGTCACAAAGTGGCCA 84

Qy 19 -----LysLysArgPheGluValLysLysSerTrpAsnAlaValAlaLeuTrpAla 34  
 Db 85 GTGGAACCAAAAGAGAGATTGAAATTGAAATTGAACTTCGTC 144

Qy 35 TrpAspIleValValAspAsnCysAlaIleCysArgAsnHisIleMetAspLeuCysIle 54  
 Db 145 TCGGATATTAGCTGTGCAACTGTGCTATTGAGAACCCATT 204

Qy 55 GluCysGlnAlaAsnGlnAlaSerAlaThrSerGluCysThrValAlaIlePrglyVal 74  
 Db 205 GATGCCAGCZAAAGGCATGACGGCATGACGGCATGATAAGATGTGAGCCTGGGTGTC 264

Qy 75 CysAsnHisAlaPheHisPheHisCysIleSerArgTrpLeuLysThrArgGlnValCys 94  
 Db 265 TGTAAATTACGCTTTCCATTGACTGATTATAATTGGATAAAGACAAGAACGCCATGTC 324

Qy 95 ProLeuAspAsnArgGluIlePheGlnLysTrpGly 107  
 Db 325 CCATTAAGATAACCAACCTTGSCAGTTAGCAAGATGGCGT 363

RESULT 14  
 US-09-248-796A-5495  
 / Sequence 5495, Application US/09248796A.  
 / Patent No. 6747137  
 / GENERAL INFORMATION:  
 / APPLICANT: Keith Weinstock et al.  
 / TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
 / FILE REFERENCE: FOR DIAGNOSTICS AND THERAPEUTICS  
 / CURRENT APPLICATION NUMBER: US/09/248,796A  
 / CURRENT FILING DATE: 1999-02-12  
 / PRIOR APPLICATION NUMBER: US 60/074,725  
 / PRIOR FILING DATE: 1998-02-13  
 / PRIOR APPLICATION NUMBER: US 60/096,409  
 / PRIOR FILING DATE: 1998-08-13  
 / SEQ ID NO: 28208  
 / LENGTH: 357  
 / TYPE: DNA  
 / ORGANISM: Candida albicans  
 / US-09-248-796A-5495

Alignment Scores:  
 Pred. No.: 3.26e-37 Length: 357  
 Score: 375.50 Matches: 62  
 Percent Similarity: 73.3% Conservative: 12  
 Best Local Similarity: 61.4% Mismatches: 26  
 Query Match: 61.0% Indels: 1  
 DB: 3 DB: 1  
 Gaps: 3

US-09-541-462B-2 (1-108) × US-09-826-312A-7 (1-342)

Qy 11 SerGlyThrAsnSerGlyAlaGlyLysLysSerGluValLysLysTrpAsnAlaVal 30  
 Db 58 TCAGGCTCAAGTCGGGA---GGGACACAGATGCTTCCTCAAGAACCTGGTG 114

Qy 31 AlaLeuTrpAlaIlePaspIleValValAspAsnCysSerGlnAlaSerAla 50  
 Db 115 GCACTGGAGCTGGACGTTGAGTGCCTGCGCATCTGAGGGTCCAGGTGATG 174

Qy 51 AspLeuCysIleGluCysGlnAlaAsnGlnAlaSerAlaThrSerGluGluCysThrVal 70  
 Db 175 GATGCTGCTTAAATGATGTCAGCTAACAC 225

Qy 71 AlaTrpGlyValCysGlnAlaPheHisPheHisCysIleSerArgTrpLeuLysThr 90  
 Db 226 GTCCTGGGGAAATGTAATCATTCTCTCCACACTGCTGCTGCGGTAAACAG 285

Qy 91 ArgGlnValCysPaspLeuAspAsnArgGluIlePheGlnLysTrpGly 107  
 Db 286 AACAAATCGTGCCTCTGCAAGGGACTGGTGGTCAAAGAAATGCGG 336

Search completed: March 11, 2006, 08:22:43  
 Job time : 137 secs

Qy 49 IleMetAspLeuCysIleGluCysGlnAlaAsn--GlnAlaSerAlaThrSerGluGlu 67  
 Db 52 ACAACGAAACAAACATCAAACCATCATCAAAACCAGATTGAGTGAATAATTGGACA 111

Qy 29 AlaValAlaLeuTrpAlaIlePaspIleValValAspAsnCysSerGlnAla 48  
 Db 112 GCGTAGCTTGGCATGGGATATGCAAAATTGAAATGTGCCATTCTGAAATCAT 171

Qy 49 IleMetAspLeuCysIleGluCysGlnAlaAsn--GlnAlaSerAlaThrSerGluGlu 67  
 Db 172 TTAATCGAACATGATGATGAACTTGCATGAACTTGCATGAACTTGCAGAAAG 231

Qy 68 CysThrIleValAlaIlePaspIlyValCysSerAsnHisAlaPheHisIleSerArgTRP 87  
 Db 232 TGTATTCCTGCTGGAGATGATGATCATGCATTCAATTGATTAGAGATGG 291

Qy 88 LeuLysThrArgGlnValCysPaspLeuAspAsnArgGluIlePheGlnLysTrpGly 107

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GenCore version 5.1.7  
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M nucleic - nucleic search, using sw model

run on: March 8, 2006, 14:30:51 ; Search time 297.184 Seconds  
 (without alignments)  
 2538.786 Million cell updates/sec

title: US-09-541-462B-1  
 perfect score: 327  
 sequence: 1 atggcggcggcgatggatgt.....tccaaasaggatggcactag 327

scoring table: Oligo-NuC  
 Gapop=60.0 , Gapext 60.0

searched: 7673375 seqs, 1153648444 residues

word size : 12

total number of hits satisfying chosen parameters: 38280

minimum DB seq length: 0  
 maximum DB seq length: 2000000000

post-processing: Listing first 45 summaries

database : Published Applications NA New:  
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 2: /cgn2\_6\_ptodata/2/pubnpna/us06 NEW\_PUB.seq: \*  
 3: /cgn2\_6\_ptodata/2/pubnpna/us07 NEW\_PUB.seq: \*  
 4: /cgn2\_6\_ptodata/2/pubnpna/pct\_NEW\_PUB.seq: \*  
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 6: /cgn2\_6\_ptodata/2/pubnpna/us09 NEW\_PUB.seq: \*  
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 12: /cgn2\_6\_ptodata/2/pubnpna/us11\_NEW\_PUB.seq4: \*  
 13: /cgn2\_6\_ptodata/2/pubnpna/us00\_NEW\_PUB.seq: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

result No.	Score	Query Match	Length	DB ID	Description
1	25	7.6	25	12 US-11-121-849-188861	Sequence 188861,
2	25	7.6	25	12 US-11-121-849-188862	Sequence 188862,
3	25	7.6	25	12 US-11-121-849-188863	Sequence 188863,
4	25	7.6	25	12 US-11-121-849-188864	Sequence 188864,
5	25	7.6	25	12 US-11-121-849-188865	Sequence 188865,
6	25	7.6	25	12 US-11-121-849-188866	Sequence 188866,
7	25	7.6	25	12 US-11-121-849-188867	Sequence 188867,
8	23	7.0	23	12 US-11-090-617-351	Sequence 351, App
9	19	5.8	19	10 US-11-101-244-692822	Sequence 692822,
10	19	5.8	19	10 US-11-101-244-692830	Sequence 692830,
11	19	5.8	19	10 US-11-101-244-692831	Sequence 692831,
12	19	5.8	19	10 US-11-101-244-692824	Sequence 692824,
13	19	5.8	19	10 US-11-101-244-692826	Sequence 692826,
14	19	5.8	19	10 US-11-101-244-692827	Sequence 692827,
15	19	5.8	19	10 US-11-101-244-692832	Sequence 692832,
16	19	5.8	19	10 US-11-101-244-692833	Sequence 692833,
17	19	5.8	19	10 US-11-101-244-692834	Sequence 692834,
18	19	5.8	19	10 US-11-101-244-692835	Sequence 692835,
19	19	5.8	19	10 US-11-101-244-692836	Sequence 692836,
20	19	5.8	19	10 US-11-101-244-692837	Sequence 692837,

ALIGNMENTS

RESULT	Query	Match	Score	25;	DB 12;	Length	25;
1	US-11-121-849-188861	Best Local Similarity	100.0%	Pred. No.	0.00063;	Indels	0;
		Matches	25;	Mismatches	0;	Gaps	
2	179 AGGGTCCGCTACTTCAGAGAGTG 203						
3	1 AGGGTCCGCTACTTCAGAGAGTG 25						

RESULTS

RESULT	Query	Match	Score	25;	DB 12;	Length	25;
2	US-11-121-849-188862	Best Local Similarity	100.0%	Pred. No.	0.00063;	Indels	0;
		Matches	25;	Mismatches	0;	Gaps	
3	179 AGGGTCCGCTACTTCAGAGAGTG 203						
4	1 AGGGTCCGCTACTTCAGAGAGTG 25						

GENERAL INFORMATION:

APPLICANT: John Palma  
 TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Tissue

FILE REFERENCE: 3684.1  
 CURRENT APPLICATION NUMBER: US/11/121,849  
 CURRENT FILING DATE: 2004-05-03  
 PRIORITY APPLICATION NUMBER: 60/567,949  
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
 NUMBER OF SEQ ID NOS: 673904  
 SEQ ID NO 188861  
 LENGTH: 25  
 TYPE: DNA  
 ORGANISM: Homo sapien

US-11-121-849-188861

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/ NUMBER OF SEQ ID NOS: 673904
/ SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/ SEQ ID NO: 188862
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-11-121-849-188862

Query Match          7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    193 TCAAGAGCTGATCTCGATGG 217
      ||||| ||||| ||||| ||||| |||
Db     1 TCAAGAGCTGATCTCGATGG 25

RESULT 3
US-11-121-849-188863
/ Sequence 188863, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/   APPLICANT: John Palma
/   TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Sequences
/   TITLE OF INVENTION: Microarrays
/   FILE REFERENCE: 3684_1
/   CURRENT APPLICATION NUMBER: US/11/121,849
/   CURRENT FILING DATE: 2005-05-03
/   PRIOR APPLICATION NUMBER: 60/567,949
/   PRIOR FILING DATE: 2004-05-03
/   NUMBER OF SEQ ID NOS: 673904
/   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/   SEQ ID NO: 188863
/   LENGTH: 25
/   TYPE: DNA
/   ORGANISM: Homo sapien
US-11-121-849-188863

Query Match          7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    246 CTGCACTCTCGCTGGCTAAACA 270
      ||||| ||||| ||||| ||||| ||||| |||
Db     1 CTGCACTCTCGCTGGCTAAACA 25

RESULT 4
US-11-121-849-188864
/ Sequence 188864, Application US/11121849
/ Publication No. US20050272080A1
/ GENERAL INFORMATION:
/   APPLICANT: John Palma
/   TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded Sequences
/   TITLE OF INVENTION: Microarrays
/   FILE REFERENCE: 3684_1
/   CURRENT APPLICATION NUMBER: US/11/121,849
/   CURRENT FILING DATE: 2005-05-03
/   PRIOR APPLICATION NUMBER: 60/567,949
/   PRIOR FILING DATE: 2004-05-03
/   NUMBER OF SEQ ID NOS: 673904
/   SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
/   SEQ ID NO: 188864
/   LENGTH: 25
/   TYPE: DNA
/   ORGANISM: Homo sapien
US-11-121-849-188864

Query Match          7.6%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.00063;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy    255 TCCCTGGTCAAAACAGACAGGTG 279
      ||||| ||||| ||||| ||||| ||||| |||

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CURRENT APPLICATION NUMBER: US/11/121,849  
; PRIORITY NUMBER: 60/567,949  
; PRIORITY FILING DATE: 2004-05-03  
; NUMBER OF SEQ ID NOS: 6739/4  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO: 188867  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-11-121-849-188867

Query Match Score 7.6%; Best Local Similarity 100.0%; Pred. No. 0.0063; Mismatches 0; Indels 0; Gaps 0;

Matches 25; Conservative 0; Gaps 0;

Qy 302 GGGAAATTCCAAAAGTAGGGCACTA 326  
Db 1 GGGAAATTCCAAAAGTAGGGCACTA 25

RESULT 8

US-11-090-617-351  
; Sequence 351, Application US/11090617  
; Publication No. US20060024692A1

GENERAL INFORMATION:

; APPLICANT: Nakamura, Yusuke  
; APPLICANT: Daigo, Yataro  
; APPLICANT: Nakatsuru, Shuichi  
; TITLE OF INVENTION: METHOD FOR DIAGNOSING NON-SMALL CELL LUNG CANCERS  
; FILE REFERENCE: 082368-003500US  
; CURRENT APPLICATION NUMBER: US/11/090,617  
; CURRENT FILING DATE: 2005-03-24  
; PRIOR APPLICATION NUMBER: PCT/JP04/04075  
; PRIOR FILING DATE: 2004-03-24  
; PRIOR APPLICATION NUMBER: PCT/JP03/12072  
; PRIOR FILING DATE: 2003-09-22  
; PRIOR APPLICATION NUMBER: US 60/555,757  
; PRIOR FILING DATE: 2004-03-24  
; PRIOR APPLICATION NUMBER: US 60/466,100  
; PRIOR FILING DATE: 2003-04-28  
; PRIOR APPLICATION NUMBER: US 60/451,374  
; PRIOR FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/414,673  
; PRIOR FILING DATE: 2002-09-30  
; NUMBER OF SEQ ID NOS: 706  
; SEQ ID NO: 351  
; LENGTH: 23  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Artificially synthesized primer sequence for RT-PCR

US-11-090-617-351

Query Match Score 7.0%; Best Local Similarity 100.0%; Pred. No. 0.0088; Mismatches 0; Indels 0; Gaps 0;

Matches 23; Conservative 0; Gaps 0;

Qy 70 GTGAAAAATGTTGAATGCACTAGTC 92  
Db 1 GTGAAAAATGTTGAATGCACTAGTC 23

RESULT 9

US-11-101-244-692822  
; Sequence 692822, Application US/11101244  
; Publication No. US20050246794A1

GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khorrova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William

Query Match Score 5.8%; Best Local Similarity 78.9%; Pred. No. 1.7%; Mismatches 4; Indels 0; Gaps 0;

Matches 15; Conservative 4; Gaps 0;

Qy 57 GAACCGCTTGTGAGTGAAA 75  
Db 1 GAACCGCTTGTGAGTGAAA 19

RESULT 11

US-11-101-244-692824  
; Sequence 692824, Application US/11101244  
; Publication No. US20050246794A1

GENERAL INFORMATION:

; APPLICANT: Dharmacon, Inc.  
; APPLICANT: Khorrova, Anastasia  
; APPLICANT: Reynolds, Angela  
; APPLICANT: Leake, Devin  
; APPLICANT: Marshall, William

APPLICANT: Scaringe, Stephen  
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 FILE REFERENCE: 13499US  
 CURRENT APPLICATION NUMBER: US/11/101,244  
 CURRENT FILING DATE: 2005-04-07  
 PRIORITY NUMBER: 60/502,050  
 PRIOR FILING DATE: 2003-09-10  
 PRIORITY APPLICATION NUMBER: 60/426,137  
 PRIORITY FILING DATE: 2002-11-14  
 NUMBER OF SEQ ID NOS: 1591911  
 SOFTWARE: Proprietary  
 SEQ ID NO: 692824  
 LENGTH: 19  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-11-101-244-692824

RESULT 12  
 US-11-101-244-692826  
 Sequence 692826, Application US/11101244  
 Publication No. US20050246794A1  
 GENERAL INFORMATION:  
 APPLICANT: Dharmacon, Inc.  
 APPLICANT: Khvorova, Anastasia  
 APPLICANT: Reynolds, Angela  
 APPLICANT: Leake, Devin  
 APPLICANT: Marshall, William  
 APPLICANT: Scaringe, Stephen  
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 FILE REFERENCE: 13499US  
 CURRENT APPLICATION NUMBER: US/11/101,244  
 CURRENT FILING DATE: 2005-04-07  
 PRIORITY NUMBER: 60/502,050  
 PRIOR FILING DATE: 2003-09-10  
 PRIORITY APPLICATION NUMBER: 60/426,137  
 PRIORITY FILING DATE: 2002-11-14  
 NUMBER OF SEQ ID NOS: 1591911  
 SOFTWARE: Proprietary  
 SEQ ID NO: 692826  
 LENGTH: 19  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-11-101-244-692826

RESULT 13  
 US-11-101-244-692827  
 Sequence 692827, Application US/11101244  
 Publication No. US20050246794A1  
 GENERAL INFORMATION:  
 APPLICANT: Dharmacon, Inc.  
 APPLICANT: Khvorova, Anastasia  
 APPLICANT: Reynolds, Angela  
 APPLICANT: Leake, Devin  
 APPLICANT: Marshall, William  
 APPLICANT: Scaringe, Stephen  
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 FILE REFERENCE: 13499US  
 CURRENT APPLICATION NUMBER: US/11/101,244  
 CURRENT FILING DATE: 2005-04-07  
 PRIORITY NUMBER: 60/502,050  
 PRIOR FILING DATE: 2003-09-10  
 PRIORITY APPLICATION NUMBER: 60/426,137  
 PRIORITY FILING DATE: 2002-11-14  
 NUMBER OF SEQ ID NOS: 1591911  
 SOFTWARE: Proprietary  
 SEQ ID NO: 692827  
 LENGTH: 19  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-11-101-244-692827

RESULT 14  
 US-11-101-244-692829  
 Sequence 692829, Application US/11101244  
 Publication No. US20050246794A1  
 GENERAL INFORMATION:  
 APPLICANT: Dharmacon, Inc.  
 APPLICANT: Khvorova, Anastasia  
 APPLICANT: Reynolds, Angela  
 APPLICANT: Leake, Devin  
 APPLICANT: Marshall, William  
 APPLICANT: Scaringe, Stephen  
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 FILE REFERENCE: 13499US  
 CURRENT APPLICATION NUMBER: US/11/101,244  
 CURRENT FILING DATE: 2005-04-07  
 PRIORITY NUMBER: 60/502,050  
 PRIOR FILING DATE: 2003-09-10  
 PRIORITY APPLICATION NUMBER: 60/426,137  
 PRIORITY FILING DATE: 2002-11-14  
 NUMBER OF SEQ ID NOS: 1591911  
 SOFTWARE: Proprietary  
 SEQ ID NO: 692829  
 LENGTH: 19  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-11-101-244-692829

RESULT 15  
 US-11-101-244-692830  
 Sequence 692830, Application US/11101244  
 Publication No. US20050246794A1  
 GENERAL INFORMATION:  
 APPLICANT: Dharmacon, Inc.  
 APPLICANT: Khvorova, Anastasia  
 APPLICANT: Reynolds, Angela  
 APPLICANT: Leake, Devin  
 APPLICANT: Marshall, William  
 APPLICANT: Scaringe, Stephen  
 TITLE OF INVENTION: Functional and Hyperfunctional siRNA  
 FILE REFERENCE: 13499US  
 CURRENT APPLICATION NUMBER: US/11/101,244  
 CURRENT FILING DATE: 2005-04-07  
 PRIORITY NUMBER: 60/502,050  
 PRIOR FILING DATE: 2003-09-10  
 PRIORITY APPLICATION NUMBER: 60/426,137  
 PRIORITY FILING DATE: 2002-11-14  
 NUMBER OF SEQ ID NOS: 1591911  
 SOFTWARE: Proprietary  
 SEQ ID NO: 692830  
 LENGTH: 19  
 TYPE: RNA  
 ORGANISM: Homo sapiens  
 US-11-101-244-692830

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; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO: 692830
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
; US-11-101-244-692830

Query Match      Score 19; DB 10; Length 19;
Best Local Similarity 84.2%; Prd. No. 1.7;
Matches 16; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Oy          134 GCACGGAAACCACATTATGGA 152
                         ||||| ||||| : : |||
Db          1 GCACGGAAACCACAUUAGGA 19

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Search completed: March 8, 2006, 14:44:48  
Job time: 297.184 sec

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GenCore version 5.1.7  
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## OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 13:59:49 ; Search time 536.691 Seconds

(without alignments)  
5038.446 Million cell updates/secTitle: US-09-541-462B-1  
Perfect score: 327  
Sequence: 1 atggcgccggatggatgt.....tccaaaggatggcactag 327Scoring table: OLIGO\_NUC  
Gapop\_60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 12

Total number of hits satisfying chosen parameters: 145515

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

## Post-processing: Listing first 45 summaries

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 2: /cgpn2_6/podata/1/pubpna/us08_pubcomb.seq;*
 3: /cgpn2_6/podata/1/pubpna/us09_pubcomb.seq;*
 4: /cgpn2_6/podata/1/pubpna/us09b_pubcomb.seq;*
 5: /cgpn2_6/podata/1/pubpna/us10_pubcomb.seq;*
 6: /cgpn2_6/podata/1/pubpna/us10b_pubcomb.seq;*
 7: /cgpn2_6/podata/1/pubpna/us10c_pubcomb.seq;*
 8: /cgpn2_6/podata/1/pubpna/us10d_pubcomb.seq;*
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10: /cgpn2_6/podata/1/pubpna/us11_pubcomb.seq;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	433	7	US-10-24-535A-43377
2	327	100.0	433	7	US-10-085-43377
3	327	100.0	453	7	US-10-24-515A-35025
4	327	100.0	453	7	US-10-085-4783A-35025
5	327	100.0	467	7	US-10-24-535A-19933
6	327	100.0	467	7	US-10-085-783A-39933
7	327	100.0	471	7	US-10-24-535A-57254
8	327	100.0	471	7	US-10-085-783A-57254
9	327	100.0	472	7	US-10-24-535A-56068
10	327	100.0	472	8	US-10-085-783A-56068
11	327	100.0	508	8	US-10-913-337-3
12	327	100.0	523	7	US-10-24-535A-46292
13	327	100.0	523	7	US-10-085-783A-46292
14	325	99.4	476	3	US-09-118-995-17191
15	321	96.2	4543	5	US-10-198-846-11311
16	308	94.2	4476	8	US-10-357-330-25604
17	296	90.5	3484	8	US-10-723-360-1383
18	296	90.5	3484	9	US-10-756-149-1357
19	296	90.5	5111	5	US-11-051-454-182
20	296	90.5	5111	10	US-10-723-360-1352
21	296	90.5	5371	8	US-10-723-360-5552
22	270	82.6	468	7	US-10-24-535A-47656
23	270	82.6	468	7	US-10-085-783A-47656

## RESULT 1

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US-10-242-535A-43377
; Sequence 43377, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; ATTORNEY OR AGENT FOR APPLICANT: Lieuw, C. C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIORITY APPLICATION NUMBER: US 10/085,783
; PRIORITY FILING DATE: 2002-02-28
; PRIORITY APPLICATION NUMBER: US 60/305,340
; PRIORITY FILING DATE: 2001-07-13
; PRIORITY APPLICATION NUMBER: US 60/275,017
; PRIORITY FILING DATE: 2001-03-12
; PRIORITY APPLICATION NUMBER: US 60/271,955
; PRIORITY FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 5894
; SOFTWARE: Patentin version 3.2
; SEQ ID NO: 43377
; LENGTH: 433
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-43377
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## ALIGNMENTS

C	24	267	81.7	5347	6	US-10-240-965-99
	25	249	76.1	3208	3	US-09-780-16-27
	26	249	76.1	3208	5	US-10-214-811-27
	27	249	76.1	3208	7	US-10-766-074-27
	28	249	76.1	3208	10	US-11-036-185-2649
	29	209	63.9	509	9	US-10-450-763-54751
	30	207	63.3	430	7	US-11-242-535A-54751
	31	207	63.3	430	7	US-10-085-783A-54751
	32	198	60.6	475	7	US-10-242-535A-50604
	33	198	60.6	475	7	US-10-085-783A-50604
	34	173	52.9	300	7	US-10-242-535A-48516
	35	173	52.9	300	7	US-10-085-783A-48516
	36	170	52.0	439	3	US-09-918-995-14771
	37	166	50.8	380	3	US-10-242-535A-1677
	38	163	49.8	370	7	US-10-242-535A-19847
	39	163	49.8	318	7	US-10-242-525733
	41	157	48.0	318	7	US-10-085-783A-25733
	42	149	45.6	666	9	US-10-450-763-22648
	43	148	45.3	486	7	US-10-242-535A-52747
	44	148	45.3	486	7	US-10-450-763-22645
	45	147	45.0	398	9	US-10-450-763-22645



Best Local Similarity 100.0%; Pred. No. 1.8e-173; Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCAGCGATGATGCCAGGGACACCCAAAGGGCAAGAAG 60  
Db 24 ATGGCGCAGGGATGTGGATACCCGAGGCAACGGCCAGAAG 83

Qy 61 CGCTTGAACTGAAAGTGAATGCAATGGCTGGATAATTGGTTGAT 120  
Db 84 CGCTTGAACTGAAAGTGAATGCAATGGCTGGATAATTGGTTGAT 143

Qy 121 AACTGGCCATCTGGAGAACCATTTGGATCTTGGATAGATGCAAGTAAACCG 180  
Db 144 AACTGGCCATCTGGAGAACCATTTGGATAGATGCAAGTAAACCG 203

Qy 181 GCGTCGGCTACTTCGAAAGGTGTACTGGCATGGATCTGTAAACCTATGGTTTCACT 240  
Db 204 GCGTCGGCTACTTCGAAAGGTGTACTGGCATGGATCTGTAAACCTATGGTTTCACT 263

Qy 241 TTCCACTGCATCTCGCTGGCTCAAACAGCACGGTGTGTCATTGGACAAGAG 300  
Db 264 TTCCACTGCATCTCGCTGGCTCAAACAGCACGGTGTGTCATTGGACAAGAG 323

Qy 301 TGGGAAATCAAAAGTAGGGCACTAG 327  
Db 324 TGGGAAATCAAAAGTAGGGCACTAG 350

RESULT 6  
US-10-085-783A-39933  
; Sequence 39933, Application US/10085783A  
; Publication No. US20040037841A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2002  
; CURRENT APPLICATION NUMBER: US/10/085-783A  
; CURRENT FILING DATE: 2002-02-28  
; PRIORITY APPLICATION NUMBER: US 60/305,340  
; PRIORITY FILING DATE: 2001-07-13  
; PRIORITY APPLICATION NUMBER: US 60/275,017  
; PRIORITY FILING DATE: 2001-03-12  
; PRIORITY APPLICATION NUMBER: US 60/271,955  
; PRIORITY FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 5894  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 39933  
; LENGTH: 467  
; TYPE: DNA  
; ORGANISM: Human  
; US-10-085-783A-39933

Query Match 100.0%; Score 327; DB 7; Length 467;  
Best Local Similarity 100.0%; Pred. No. 1.8e-173;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGGCAGGGATACCCGAGGGATACCCGAGGGCACCACGGGGGAGAAG 60  
Db 20 ATGGGGCAGGGATACCCGAGGGATACCCGAGGGCACCACGGGGGAGAAG 79

Qy 61 CGTTGAAATGAAAAAGTGGAAATGCAATGGCCCTCTGGGCTGGATATTGGTTGAT 120  
Db 80 CGTTGAAATGAAAAAGTGGAAATGCAATGGCCCTCTGGGCTGGATATTGGTTGAT 139

Qy 121 AACGTGGCACTCGATGGATGATGGGATACCCGAGGGCACCACGGGGAGAAG 180  
Db 140 AACGTGGCACTCGATGGATGATGGGATACCCGAGGGCACCACGGGGAGAAG 199

Qy 181 CGCTTGAACTTGGCTCAAAGTAGGGCACTAG 327  
Db 200 CGCTTGAACTTGGCTCAAAGTAGGGCACTAG 346

RESULT 7  
US-10-242-535A-57254  
; Sequence 57254, Application US/10242535A  
; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; INVENTION: Compositions and Methods Relating to Osteoarthritis

Query Match 100.0%; Score 327; DB 7; Length 467;  
Best Local Similarity 100.0%; Pred. No. 1.8e-173;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGGGCAGGGATACCCGAGGGATACCCGAGGGCACCACGGGGAGAAG 60  
Db 20 ATGGGGCAGGGATACCCGAGGGATACCCGAGGGCACCACGGGGAGAAG 79

Qy 61 CGCTTGAACTTGGCTCAAAGTAGGGCACTAG 120  
Db 80 CGCTTGAACTTGGCTCAAAGTAGGGCACTAG 139

Qy 121 AACGTGGCACTCGATGGATGATGGGATACCCGAGGGCACCACGGGGAGAAG 180  
Db 140 AACGTGGCACTCGATGGATGATGGGATACCCGAGGGCACCACGGGGAGAAG 199

Qy 181 CGCTTGAACTTGGCTCAAAGTAGGGCACTAG 240

FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; CURRENT FILING DATE: 2002-09-12  
; PRIOR APPLICATION NUMBER: US 10/085,783  
; PRIOR FILING DATE: 2001-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
SEQ ID NO 57254  
LENGTH: 471  
; TYPE: DNA  
ORGANISM: Human  
US-10-242-535A-57254

Query Match 100.0%; Score 327; DB 7; Length 471;  
Best Local Similarity 100.0%; Pred. No. 1.8e-173;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCAGGATGGATGGTGAATCCAGGCCAACAGGGCAAGAAG 60  
Db 17 ATGGGCAGGATGGATGGTGAATCCAGGCCAACAGGGCAAGAAG 76  
Qy 61 CGCTTGAAGTAAAGTGAATGGATGGCTGGGATATTGGTTGAT 120  
Db 77 CGCTTGAAGTAAAGTGAATGGATGGCTGGGATATTGGTTGAT 136

Qy 1 ATGGCGCAGGATGGATGGTGAATCCAGGCCAACAGGGCAAGAAG 60  
Db 17 ATGGGCAGGATGGATGGTGAATCCAGGCCAACAGGGCAAGAAG 76  
Qy 61 CGCTTGAAGTAAAGTGAATGGACTAGGCCCTCTGGCTGGGATATTGGTTGAT 120  
Db 77 CGCTTGAAGTAAAGTGAATGGACTAGGCCCTCTGGCTGGGATATTGGTTGAT 136

Query Match 100.0%; Score 327; DB 7; Length 471;  
Best Local Similarity 100.0%; Pred. No. 1.8e-173;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCAGGATGGATGGTGAATCCAGGCCAACAGGGCAAGAAG 60  
Db 17 ATGGGCAGGATGGATGGTGAATCCAGGCCAACAGGGCAAGAAG 76  
Qy 61 CGCTTGAAGTAAAGTGAATGGACTAGGCCCTCTGGCTGGGATATTGGTTGAT 120  
Db 77 CGCTTGAAGTAAAGTGAATGGACTAGGCCCTCTGGCTGGGATATTGGTTGAT 136

RESULT 9  
US-10-242-535A-56068  
; Sequence 56068, Application US/10242535A  
; Publication No. US20040013663A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; INVENTOR: Lieuw, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2005  
; CURRENT APPLICATION NUMBER: US/10/242,535A  
; CURRENT FILING DATE: 2002-09-12  
; PRIORITY NUMBER: US 10/085,783  
; PRIORITY NUMBER: 2002-02-28  
; PRIORITY NUMBER: US 60/305,340  
; PRIORITY NUMBER: 2001-07-13  
; PRIORITY NUMBER: US 60/275,017  
; PRIORITY NUMBER: 2001-03-12  
; PRIORITY NUMBER: US 60/271,955  
; PRIORITY NUMBER: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
SEQ ID NO 56068  
LENGTH: 472  
; ORGANISM: Human  
; FEATURE: misc feature  
; NAME/KEY: (437).  
; LOCATION: (437).  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: (455).  
; LOCATION: (455).  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-242-535A-56068

Query Match 100.0%; Score 327; DB 7; Length 472;  
Best Local Similarity 100.0%; Pred. No. 1.8e-173;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCAGGATGGATGGTGAATCCAGGCCAACAGGGCAAGAAG 60  
Db 20 ATGGGCAGGATGGATGGTGAATCCAGGCCAACAGGGCAAGAAG 76  
Qy 61 CGCTTGAAGTAAAGTGAATGGACTAGGCCCTCTGGCTGGGATATTGGTTGAT 120  
Db 77 CGCTTGAAGTAAAGTGAATGGACTAGGCCCTCTGGCTGGGATATTGGTTGAT 136

RESULT 8  
US-10-085-783A-57254  
; Sequence 57254, Application US/10085783A  
; Publication No. US20040037841A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; INVENTOR: Lieuw, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2002  
; CURRENT APPLICATION NUMBER: US/10/085,783A  
; CURRENT FILING DATE: 2002-02-28  
; PRIORITY NUMBER: US 60/305,340  
; PRIORITY NUMBER: 2001-07-13  
; PRIORITY NUMBER: US 60/275,017  
; PRIORITY NUMBER: 2001-03-12  
; PRIORITY NUMBER: US 60/271,955  
; PRIORITY NUMBER: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
SEQ ID NO 57254  
LENGTH: 471  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (437).  
; OTHER INFORMATION: n is a, c, g, or t  
; FEATURE:  
; NAME/KEY: (455).  
; LOCATION: (455).  
; OTHER INFORMATION: n is a, c, g, or t  
US-10-085-783A-57254

Query Match 100.0%; Score 327; DB 7; Length 471;  
Best Local Similarity 100.0%; Pred. No. 1.8e-173;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCAGGATGGATGGTGAATCCAGGCCAACAGGGCAAGAAG 60  
Db 20 ATGGGCAGGATGGATGGTGAATCCAGGCCAACAGGGCAAGAAG 76  
Qy 61 CGCTTGAAGTAAAGTGAATGGACTAGGCCCTCTGGCTGGGATATTGGTTGAT 120  
Db 77 CGCTTGAAGTAAAGTGAATGGACTAGGCCCTCTGGCTGGGATATTGGTTGAT 136





Db 194 CTGTCGCATCTGCGAACCACTATTGGATCTTGCATAAGCTAACCGGC 253  
 Qy 183 GTCGCCCTACTTCAGAAAGTGACTGTGGCATGGGAATGGTAACCTGCTTCACTT 242  
 Db 254 GTCCGCTACTTCAGAAGTGACTGTGGATGGGAATGGTAACCTGCTTCACTT 313  
 Qy 243 CCACTGCACTCTCGCTGGTCAAAACAGACAGTGTCATGGACAACAGAGTG 302  
 Db 314 CCACTGCACTCTCGCTGGTCAAAACAGACAGTGTCATGGACAACAGAGTG 373  
 Qy 303 GGAATTCCAAAGATGGGACTAG 327  
 Db 374 GGAATTCCAAAGATGGGACTAG 398

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RESULT 15  
 US-10-198-846-11311/c  
 ; Sequence 11311, Application US/10198846  
 ; Publication No. US20030039974A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Lillie, James  
 ; APPLICANT: Xu, Yongyao  
 ; APPLICANT: Wang, Youzhen  
 ; STEINMANN, Kathleen  
 ; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 ; FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 ; TREATMENT OF BREAST CANCER  
 ; FILE REFERENCE: MRI-049  
 ; CURRENT APPLICATION NUMBER: US/10/198, 846  
 ; CURRENT FILING DATE: 2002-07-18  
 ; PRIOR APPLICATION NUMBER: 60/306, 220  
 ; PRIOR FILING DATE: 2001-07-18  
 ; NUMBER OF SEQ ID NOS: 14084  
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0  
 ; SEQ ID NO 11311  
 ; LENGTH: 4543  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 us-10-198-846-11311

Query Match 98.2%; Score 321; DB 5; Length 4543;  
 Best Local Similarity 100.0%; Pred. No. 4.3e-170; Mismatches 0; Indels 0; Gaps 0;  
 Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCAGCGATGGATGTGGATACCCAGCGCCACCAAAGCGCGGGAAAGGGCTTT 66  
 Db 1085 GCACCGATGGATGTGGATACCCAGCGCCACCAAAGCGCGGGAAAGGGCTTT 1026  
 Qy 67 GAAGTGAAAAAGTGAATGCACTGAGCTGGCCCTCTGGGCTGGATAATTGGCTTGATAACCTGT 126  
 Db 1025 GAAGTGAAAAAGTGAATGCACTGAGCTGGGACTCTGGCTGGGATATTGGCTTGATAACCTGT 966  
 Qy 127 GCCATCTGAGGACCACTATTGGATCTTGCATAAGATGCACTGAAACGGGCTCC 186  
 Db 965 GGCATCTGAGGACCACTATTGGATCTTGCATAAGATGCACTGAAACGGGCTCC 906  
 Qy 187 GCTACTTCAAGAAGTGACTGTGGCATGGGAGTCGGAACTCATGGTTTCACTTCAC 246  
 Db 905 GCTACTTCAAGAAGTGACTGTGGCATGGGAGTCGGAACTCATGGTTTCACTTCAC 846  
 Qy 247 TGCATCTCTGGCTGCTCAAACAGCAAGGTGTCATTGGACAACAGAGTGCGGAA 306  
 Db 845 TGCATCTCTGGCTGCTCAAACAGCAAGGTGTCATTGGACAACAGAGTGCGGAA 786  
 Qy 307 TTCCAAAATATGGGCACTAG 327  
 Db 785 TTCCAAAATATGGGCACTAG 765

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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 13:03:41 ; Search time 112.91 Seconds  
(without alignments)  
5148.003 Million cell updates/sec

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Sequence: 1 atgcggcagcgatggatgt.....tccaaaatggcactag 327

Scoring table: OLIGO\_NUC  
Gapext: 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 12

Total number of hits satisfying chosen parameters: 26735

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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8:	/cgcn2_6_ptodata/1/ina/RE_COMB_seq:*
9:	/cgcn2_6_ptodata/1/ina/backfile1_seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	482	3	US-09-513-999C-3894 Sequence 3894, AP
2	327	100.0	507	3	US-09-949-016-4940 Sequence 4940, AP
3	327	100.0	508	3	US-09-914-324A-3 Sequence 3, Appli
4	249	76.1	3208	3	US-09-780-16-27 Sequence 27, Appli
5	249	76.1	3208	3	US-10-214-811-27 Sequence 27, Appli
6	249	76.1	3208	3	US-10-766-074-27 Sequence 27, Appli
7	170	52.0	402	3	US-09-513-999C-10371 Sequence 10371, A
8	170	52.0	463	3	US-09-621-976-15180 Sequence 15180, A
9	89	27.2	25274	3	US-09-949-016-16682 Sequence 16682, A
10	50	15.3	504	3	US-09-914-324A-5 Sequence 5, Appli
11	36	11.0	601	3	US-09-949-016-174803 Sequence 174803, AP
12	20	6.1	411	3	US-09-640-211A-1731 Sequence 1731, AP
c 13	18	5.5	902	3	US-09-270-767-36361 Sequence 26361, A
c 14	18	5.5	3183	2	Sequence 10881, A
c 15	18	5.5	3183	2	Sequence 1, Appli
c 16	18	5.5	3187	6	PCT-US95-06815-1 Sequence 1, Appli
c 17	18	5.5	3192	2	US-08-706-037-26 Sequence 26, Appli
c 18	18	5.5	3192	2	US-08-940-661A-1 Sequence 1, Appli
c 19	18	5.5	3192	2	US-09-083-485-1 Sequence 26, Appli
c 20	18	5.5	3192	2	US-09-005-397-26 Sequence 26, Appli
c 21	18	5.5	4118	2	Sequence 3, Appli
c 22	18	5.5	63563	3	Sequence 33, Appli
c 23	18	5.5	113283	3	Sequence 1676, A
c 24	18	5.5	113283	3	Sequence 16377, A

## ALIGNMENTS

RESULT 1  
US-09-513-999C-3894  
; Sequence 3894, Application US/09513999C  
; Patent No. 6783361  
; GENERAL INFORMATION:  
; APPLICANT: Dumais Milne Edwards, J.B.  
; ATTORNEY: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783361  
; FILE REFERENCE: 5.9\_us2.REG  
; CURRENT FILING DATE: 2000-02-24  
; PRIORITY APPLICATION NUMBER: US/09/513,999C  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pmm  
SEQ ID NO 3894  
LENGTH: 482  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 29..352  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 401  
; OTHER INFORMATION: r=a or g  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 404  
; OTHER INFORMATION: m=a or c  
US-09-513-999C-3894

Query Match Score 327; DB 3; Length 482;  
Best local Similarity 100.0%; Score 327;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 29 ATGGCGGAGCGATGGTGTGATACCCGAGCGCACCAACGGCGGAGAAGAG 88  
Qy 61 CGCTTGAGTGAATGAAAGTGAATGCACTGGCTCTGGCCCTCTGGCTGTGAT 120  
Db 89 CGCTTGAGTGAATGAAAGTGAATGCACTGGCTCTGGCCCTCTGGCTGTGAT 148  
Qy 121 AACGTGCCCCATCTGGAGAACACATTATGGATCTTGCATGGATTCAGCTAACCGAG 180

Db 149 AACTGTGCCATCTGAGAACCATTTATGGATTAAGTCAACCG 208  
 Qy 181 GCGTCGGCTACTTCAGAAGGTGACTCTGCATGGGAGTCATGCTTAC 240  
 Db 209 GCGTCGGCTACTTCAGAAGGTGACTCTGCATGGGAGTCATGCTTAC 268  
 Db 241 TTCCACTGATCTCTCGTGGCTAAACACGACGGTGTCAATTGACAACAGAG 300  
 Qy 269 TTCCACTGATCTCTCGTGGCTAAACACGACGGTGTCAATTGACAACAGAG 328  
 Db 301 TGGGAATTCCAAGTATGGCACTAG 327  
 Qy 329 TGGGAATTCCAAGTATGGCACTAG 355

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RESULT 2  
 US-09-949-016-4940 Application US/09949016  
 ; Patent No. 6812339

; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CLO001307  
 ; CURRENT APPLICATION NUMBER: US/09/949, 016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 4940  
 ; LENGTH: 507  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-949-016-4940

Query Match Score 327; DB 3; Length 507;  
 Best Local Similarity 100.0%; Prod. No. 7.3e-167;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ATGGGGCAGCGATGGATGGATGGATAACCCGAGGGCACCACGGCCGGAGAAG 60  
 Db 7 ATGGGGCAGCGATGGATGGATAACCCGAGGGCACCACGGCCGGAGAAG 66

Qy 1 ATGCTTGAACTGAAAAAGTGAATGCACTAGCCCTCTGGCCCTGGATATTGGCTTGAT 120  
 Qy 61 CGCTTTGAACTGAAAAAGTGAATGCACTAGCCCTCTGGCCCTGGATATTGGCTTGAT 120  
 Db 67 CGCTTTGAACTGAAAAAGTGAATGCACTAGCCCTCTGGCCCTGGATATTGGCTTGAT 126

Db 121 AACGTGCCATCTGGAGGACCAATTGGATGATGATGCTAACGTAACCGAG 180  
 Db 127 AACGTGCCATCTGGAGGACCAATTGGATGATGATGCTAACGTAACCGAG 186

Qy 181 GCGTCGGTACTTCAGAAGGTGACTGTGCAATTGGATGCTAACGTAACCGAG 186  
 Db 187 GCGTCGGTACTTCAGAAGGTGACTGTGCAATTGGATGCTAACGTAACCGAG 186

Db 241 TTCCACTGATCTCTCGTGGCTAAACACGACGGTGTCAATTGACAACAGAG 300  
 Qy 61 CGCTTTGAACTGAAAAAGTGAATGCACTAGCCCTCTGGCCCTGGATATTGGCTTGAT 120  
 Db 67 CGCTTTGAACTGAAAAAGTGAATGCACTAGCCCTCTGGCCCTGGATATTGGCTTGAT 126

Qy 121 AACGTGCCATCTGGAGGACCAATTGGATGATGATGCTAACGTAACCGAG 180  
 Db 127 AACGTGCCATCTGGAGGACCAATTGGATGATGATGCTAACGTAACCGAG 186

RESULT 4  
 US-09-780-016-27 Application US/097800016  
 ; Sequence 27, Application US/097800016  
 ; Patent No. 6509456  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donoho, Gregory  
 ; APPLICANT: Scoville, John  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Friedrich, Glenn  
 ; APPLICANT: Abuin, Alejandro  
 ; APPLICANT: Zambrowicz, Brian  
 ; APPLICANT: Saada, Arthur T.  
 ; TITLE OF INVENTION: No. 6509456 Human Proteases and Polynucleotides Encoding the Same  
 ; TITLE OF INVENTION: LEX-0132-USA  
 ; FILE REFERENCE: US-09-914-324A-3  
 ; CURRENT APPLICATION NUMBER: US/09/780,016  
 ; CURRENT FILING DATE: 2001-02-09

RESULT 3  
 US-09-914-324A-3 Application US/09914324A  
 ; Sequence 3, Application US/09914324A

PRIOR APPLICATION NUMBER: US 60/181,294	
PRIOR FILING DATE: 2000-02-11	
NUMBER OF SEQ ID NOS: 27	
SOFTWARE: FastSEQ for Windows Version 4.0	
SEQ ID NO: 27	
LENGTH: 3208	
TYPE: DNA	
ORGANISM: homo sapiens	
US-09-780-016-27	
Query Match	76.1%; Score 249; DB 3; Length 3208;
Best Local Similarity	100.0% ; Pred. No. 1.3e-12; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 0;	
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Qy	139 AACCAATTGGATCTTGATAGAATGTCAGCTAACAGCTAACTCGAGA 198
Db	2776 TGGATGAGTAGCCCTGGGATATGTGGTATACTGCCATCTGGAGG 2835
RESULT 6	
	; Sequence 27, Application US/10766074
	; Patent No. 6881563
	; GENERAL INFORMATION:
	; APPLICANT: Donoho, Gregory
	; APPLICANT: Scoville, John
	; APPLICANT: Turner, C. Alexander Jr.
	; APPLICANT: Friedrich, Glenn
	; APPLICANT: Abuin, Alejandro
	; APPLICANT: Zambrowicz, Brian
	; APPLICANT: Sands, Arthur T.
	; TITLE OF INVENTION: No. 6881563el Human Proteases and Polynucleotides Encoding the Same
	; FILE REFERENCE: LEX-0132-USA
	; CURRENT APPLICATION NUMBER: US/10/766,074
	; CURRENT FILING DATE: 2004-01-28
	; PRIOR APPLICATION NUMBER: US/10/214,811
	; PRIOR FILING DATE: 2002-08-07
	; PRIORITY NUMBER: US/09/780,016
	; PRIORITY NUMBER: LEX-0132-09
	; PRIORITY FILING DATE: 2001-02-09
	; PRIORITY APPLICATION NUMBER: US 60/181,294
	; PRIORITY FILING DATE: 2000-02-11
	; NUMBER OF SEQ ID NOS: 27
	; SOFTWARE: FastSEQ for Windows Version 4.0
	; SEQ ID NO: 27
	; LENGTH: 3208
	; TYPE: DNA
	; ORGANISM: homo sapiens
	US-10-766-074-27
RESULT 5	
	; Sequence 27, Application US/10214811
	; Patent No. 6741621
	; GENERAL INFORMATION:
	; APPLICANT: Donoho, Gregory
	; APPLICANT: Scoville, John
	; APPLICANT: Turner, C. Alexander Jr.
	; APPLICANT: Friedrich, Glenn
	; APPLICANT: Abuin, Alejandro
	; APPLICANT: Zambrowicz, Brian
	; APPLICANT: Sands, Arthur T.
	; TITLE OF INVENTION: No. 6743621el Human Proteases and Polynucleotides Encoding the Same
	; FILE REFERENCE: LEX-0132-USA
	; CURRENT APPLICATION NUMBER: US/10/214,811
	; CURRENT FILING DATE: 2002-08-07
	; PRIORITY NUMBER: US/09/780,016
	; PRIORITY FILING DATE: 2001-02-09
	; PRIORITY APPLICATION NUMBER: US 60/181,294
	; PRIORITY FILING DATE: 2000-02-11
	; NUMBER OF SEQ ID NOS: 27
	; SOFTWARE: FastSEQ for Windows Version 4.0
	; SEQ ID NO: 27
	; LENGTH: 3208
	; TYPE: DNA
	; ORGANISM: homo sapiens
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Query Match	76.1%; Score 249; DB 3; Length 3208;
Best Local Similarity	100.0% ; Pred. No. 1.3e-12; Indels 0; Gaps 0;
Matches 249; Conservative 0; Mismatches 0;	
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Db	2776 TGGATGAGTAGCCCTGGGCTCTGGGCTCTGGGATATGTGGTATACTGCCATCTGCAGG 138
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US-09-621-976-15180  
Sequence 10371, Application US/09513999C  
Patent No. 6783965  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
ATTORNEY: Ductert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
Patent No. 6783961  
FILE REFERENCE: 59-US2-REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/1122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent-ppm  
SEQ ID NO 10371  
LENGTH: 402  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 20  
OTHER INFORMATION: k=g or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 38  
OTHER INFORMATION: s=g or c  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 79  
OTHER INFORMATION: n=a, g, c or t  
Query Match 52.0%; Score 170; DB 3; Length 402;  
Best Local Similarity 100.0%; Pred. No. 6.8e-82;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 158 GCATAGAATGCAAGTAACTGGCTTCACTTCACCTCGGTACTCTGGCATGGG 217  
Db 106 GCATAGAATGCAAGTAACTGGCTTCACTTCACCTCGGTACTCTGGCATGGG 165  
Qy 218 GAGTCTGTAACCTGGCTTCACTTCACCTCGGTACTCTGGCATGGG 277  
Db 166 GAGTCTGTAACCTGGCTTCACTTCACCTCGGTACTCTGGCATGGG 225  
Qy 278 TGTGTCATTCGACACAGAGTGGGAATTCCAAAAGTTGGCCTAG 327  
Db 226 TGTGTCATTCGACACAGAGTGGGAATTCCAAAAGTTGGCCTAG 275  
RESULT 8  
US-09-621-976-15180  
Sequence 15180, Application US/09621976  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
ATTORNEY: Jobert, S.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET 054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent-ppm  
SEQ ID NO 15180  
LENGTH: 463  
TYPE: DNA  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: n=a, g, c or t  
Query Match 52.0%; Score 170; DB 3; Length 463;  
Best Local Similarity 100.0%; Pred. No. 6.9e-82;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 158 GCATAGAATGCAAGTAACTGGCTTCACTTCACCTCGGTACTCTGGCATGGG 217  
Db 101 GCATAGAATGCAAGTAACTGGCTTCACTTCACCTCGGTACTCTGGCATGGG 160  
Qy 218 GAGTCTGTAACCTGGCTTCACTTCACCTCGGTACTCTGGCATGGG 277  
Db 161 GAGTCTGTAACCTGGCTTCACTTCACCTCGGTACTCTGGCATGGG 220  
Qy 278 TGTGTCATTCGACACAGAGTGGGAATTCCAAAAGTTGGCCTAG 327  
Db 221 TGTGTCATTCGACACAGAGTGGGAATTCCAAAAGTTGGCCTAG 270  
RESULT 9  
US-09-949-016-16682  
Sequence 16682, Application US/09949016  
PATENT NO. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO 16682  
LENGTH: 25274  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-16682  
Query Match 27.2%; Score 89; DB 3; Length 25274;  
Best Local Similarity 100.0%; Pred. No. 5.4e-38;  
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 229 CATGCTTTCACTTCACCTCGATCTCGTGGCTAACAGAGGTGTCCATTG 288  
Db 18411 CATGCTTTCACTTCACCTCGATCTCGTGGCTAACAGAGGTGTCCATTG 18470  
Qy 289 GACAACGAGAGTGGGAATTCCAAAAGTA 317  
Db 18471 GACAACGAGAGTGGGAATTCCAAAAGTA 18499  
RESULT 10  
US-09-914-324A-5  
Sequence 5, Application US/09914324A  
PATENT NO. 6838709  
GENERAL INFORMATION:  
APPLICANT: Conaway, Joan A.  
ATTORNEY: Conaway, Ronald C.  
APPLICANT: Kamura, Takumi  
APPLICANT: Okamura Medical Research Foundation  
TITLE OF INVENTION: No. 6838709-1 Component of von Hippel-Lindau Tumor Suppressor Ligase  
FILE REFERENCE: 021044-004600US  
CURRENT APPLICATION NUMBER: US/09/914,324A  
CURRENT FILING DATE: 2003-02-11  
PRIOR APPLICATION NUMBER: US 60/121,787  
PRIOR FILING DATE: 1999-02-14

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; PRIOR APPLICATION NUMBER: WO_PCT/US00/04838
; PRIOR FILING DATE: 2000-02-15
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 5
; LENGTH: 504
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (18)..(344)
; OTHER INFORMATION: Rbx1
US-09-914-324A-5

Query Match      15.3%;  Score 50;  DB 3;  Length 504;
Best Local Similarity 100.0%;  Pred. No. 6.1e-17;
Matches 50;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   109 ATTGCGGTGATAACTGTGCCATCAGGAAACCATATTGGATCTTG 158
Db   126 ATTGCGGTGATAACTGTGCCATCAGGAAACCATATTGGATCTTG 175
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                                         US-09-270-767-26361/C
                                         ; Sequence 26361, Application US/09270767
                                         ; Patent No. 6703491
                                         ; GENERAL INFORMATION:
                                         ; APPLICANT: Homburger et al.
                                         ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
                                         ; FILE REFERENCE: File Reference: 7326-094
                                         ; CURRENT APPLICATION NUMBER: US/09/270,767
                                         ; NUMBER OF SEQ ID NOS: 62517
                                         ; SOFTWARE: PatentIn Ver. 2.0
                                         ; SEQ ID NO: 26361
                                         ; LENGTH: 287
                                         ; TYPE: DNA
                                         ; ORGANISM: Drosophila melanogaster
                                         ; FEATURE:
                                         ; OTHER INFORMATION: n means any nucleotide
                                         US-09-270-767-26361

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                                         Best Local Similarity 100.0%;  Pred. No. 12.3e-01;
                                         Matches 18;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy   299 AGTGGAAATTCCAAGT 316
Db   113 AGTGGAAATTCCAAGT 96
                                         RESULT 14
                                         US-09-270-767-10881/C
                                         ; Sequence 10881, Application US/09270767
                                         ; Patent No. 6703491
                                         ; GENERAL INFORMATION:
                                         ; APPLICANT: Homburger et al.
                                         ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
                                         ; FILE REFERENCE: File Reference: 7326-094
                                         ; CURRENT APPLICATION NUMBER: US/09/270,767
                                         ; NUMBER OF SEQ ID NOS: 62517
                                         ; SOFTWARE: PatentIn Ver. 2.0
                                         ; SEQ ID NO: 10881
                                         ; LENGTH: 902
                                         ; TYPE: DNA
                                         ; ORGANISM: Drosophila melanogaster
                                         ; FEATURE:
                                         ; OTHER INFORMATION: n means any nucleotide
                                         US-09-270-767-10881

                                         Query Match      5.5%;  Score 18;  DB 3;  Length 902;
                                         Best Local Similarity 100.0%;  Pred. No. 13.0e-01;
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Qy   299 AGTGGAAATTCCAAGT 316

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Db 728 AGTGGGATTCCAAAAGT 711

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RESULT 15  
US-08-939-218A-1/c  
Sequence 1, Application US/08939218A  
Patent No. 5981243

GENERAL INFORMATION:

APPLICANT: BERKA, Randy Michael  
APPLICANT: BROWN, Stephen H.  
APPLICANT: XU, Feng  
APPLICANT: SCHNEIDER, Palle  
APPLICANT: OXENBLL, Karen M.  
APPLICANT: AASLING, Dorrit A.  
TITLE OF INVENTION: PURIFIED MYCETOLOPHTHORA LACCASES AND NUCLEIC ACIDS ENCODING SAME

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: No. 5981243o No. 5981243disk of No. 5981243th America, Inc.  
STREET: 405 Lexington Avenue, 64th Floor  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10174-6401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/939,218A  
FILING DATE: 29-SEPT-1997  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Rozek, Carol E.  
REGISTRATION NUMBER: 36,993  
REFERENCE/DOCKET NUMBER: 4184.120-US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 212-667-0123  
TELEFAX: 212-878-9655

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 3183 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS  
LOCATION: join(586..831, 917..994, 1079..1090, 1193..1264,  
US-08-939-218A-1

Query Match 5.5%; Score 18; DB 2; Length 3183;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	198 AGAGTGTACTGTGGATG	215
Db	924 AGAGTGTACTGTGGATG	907

Search completed: March 8, 2006, 14:34:35  
Job time : 114.91 secs

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CM nucleic - nucleic search, using sw model

Run on: March 15, 2006, 10:15:10 ; Search time 3736 Seconds  
(without alignments)  
4095.122 Million cell updates/sec

Title: US-09-541-462B-1

Perfect score: 327

Sequence: 1 atggccggatggatgt.....tccaaatggcactag 327

Scoring table: OLIGO\_NUC

Gapext\_60.0 Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 12

Total number of hits satisfying chosen parameters: 897482

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :	EST*	EST*
	1: 9b_est1:*	1: 9b_est1:*
	2: 9b_est2:*	2: 9b_est2:*
	3: 9b_est3:*	3: 9b_est3:*
	4: 9b_hrc:*	4: 9b_hrc:*
	5: 9b_est4:*	5: 9b_est4:*
	6: 9b_est5:*	6: 9b_est5:*
	7: 9b_est6:*	7: 9b_est6:*
	8: 9b_est7:*	8: 9b_est7:*
	9: 9b_gsa1:*	9: 9b_gsa1:*
	10: 9b_gss2:*	10: 9b_gss2:*
	11: 9b_gss3:*	11: 9b_gss3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	327	100.0	462	7 CN305890	CN305890 170005830
2	327	100.0	471	2 BG339057	BG339057 60436882
3	327	100.0	473	5 BX283972	BX283972 BX283972
4	327	100.0	488	2 BG777485	BG777485 602664820
5	327	100.0	498	6 CB296618	CB296618 1.B22006
6	327	100.0	509	7 CN305892	CN305892 170005001
7	327	100.0	518	3 BP420485	BP420485 BP420485
8	327	100.0	522	1 AL711573	AL711573 DKFZp686I
9	327	100.0	525	2 BG337472	BG337472 602435003
10	327	100.0	527	3 BM715215	BM715215 UI-E-CL1-
11	327	100.0	527	5 BU932751	BU932751 AGENCOURT
12	327	100.0	527	6 CB997822	CB997822 AGENCOURT
13	327	100.0	529	3 BM757406	BM757406 K-EST036
14	327	100.0	529	6 CD523457	CD523457 AGENCOURT
c 15	327	100.0	533	5 BUT29963	BUT29963 UI-E-CKL-
16	327	100.0	537	2 BG4786522	BG4786522 60255509
17	327	100.0	546	5 BU941262	BU941262 AGENCOURT
18	327	100.0	546	2 BI198015	BI198015 602762132
19	327	100.0	546	5 BU601181	BU601181 AGENCOURT
20	327	100.0	548	1 AV16338	AV16338 AV16338
21	327	100.0	548	5 BU601301	BU601301 AGENCOURT
22	327	100.0	549	3 BI858425	BI858425 603386437

## ALIGNMENTS

RESULT 1  
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LOCUS  
DEFINITION 17000583044616 GRN\_PRBHEP Homo sapiens cDNA 5', mRNA sequence.  
ACCESSION CN305890  
VERSION CN305890.1 GI:412232304  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo  
1 (bases 1 to 462)

REFERENCE  
AUTHORS Brandenberger,R., Wei,R., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Li,Y., Xu,C., Pang,R., Guegler,K., Rao,M.S., Mandalam,R., Lebkowski,J. and Stanton,L.W.  
TITLE Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation  
JOURNAL Nat. Biotechnol. 22 (6), 707-716 (2004)  
PUBMED 15146197  
COMMENT Contact: Brandenberger R  
Regenerative Medicine  
Geron Corporation  
230 Constitution Drive, Menlo Park, CA 94025, USA  
Source  
FEATURES  
1. .462  
/clone lib="GRN\_PRBHEP"  
/mol type="mRNA"  
/db Xref="taxon:3606"  
/tissue type="embryonic stem cells, DMSO-treated H9 cell line"  
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Best Local Similarity 100.0%; Pred. No. 6.6e-175;  
Matches 327; Conservative 0; Mismatches 0; Gaps 0;

Qy	1 ATGGCGCAGGGATGGATGTGGATACCCGAGCCAACAGGGGGAAAGAG 60	Query Match 100.0%; Score 327; DB 2;
Db	23 ATGGCGCAGGGATGGATGTGGATACCCGAGCCAACAGGGGGAAAGAG 82	Best Local Similarity 100.0%; Pred. No. 6.e-175; Mismatches 0; Indels 0; Gaps 0;
Qy	61 CGCTTGAAGTGAAGTGAATGGAAATGCAATGCCCTCTGGCATTTGGTGTAT 120	Matches 327; Conservative 0;
Db	83 CGCTTGAAGTGAAGTGAATGGAAATGCAATGCCCTCTGGCATTTGGTGTAT 142	1 ATGGCGCAGGGATGGATGTGGATACCCGAGCCAACAGGGGGAAAGAG 60
Qy	121 AACTGTCGCCATTCTGAGGAGCCATTAATGATCTTGATAGATGTAACCG 180	Db 42 ATGGCGCAGGGATGGATGTGGATACCCGAGCCAACAGGGGGAAAGAG 101.
Qy	181 CGGTCCGCTACTTCAGAAGAGTGTACTGTCGGACTCTGTAAACATGTTTCAC 240	61 CGCTTGAAGTGAAGTGAATGGAAATGCAATGCCCTCTGGCATTTGGTGTAT 120
Db	203 CGTCCGCTACTTCAGAAGAGTGTACTGTCGGACTCTGTAAACATGTTTCAC 262	Qy 102 CGCTTGAAGTGAAGTGAATGGAAATGCAATGCCCTCTGGCATTTGGTGTAT 161.
Qy	241 TTCCACTGCATCTCGCTGCTCAAACACGACAGGTGTCCATTGGACAACAGAG 300	121 AACGTGCCATCTCAGGACCAATTGGATTTGGATAGATGTCAGCTAACCG 180
Db	263 TTCCACTGCATCTCGCTGCTCAAACACGACAGGTGTCCATTGGACAACAGAG 322	Db 162 AACGTGCCATCTCAGGACCAATTGGATTTGGATAGATGTCAGCTAACCG 221.
Qy	301 TGGGAATTCAAAAGTAGTGGCACTAG 327	Qy 181 GCGTCGCCGTACTTCAGAAGAGTGTACTGTCGGACTCTGTAAACATGTTTCAC 240
Db	323 TGGGAATTCAAAAGTAGTGGCACTAG 349	Db 222 GCGTCGCCGTACTTCAGAAGAGTGTACTGTCGGACTCTGTAAACATGTTTCAC 281
		241 TTCCACTGCATCTCGCTGCTCAAACACGACAGGTGTCCATTGGACAACAGAG 300
		282 TTCCACTGCATCTCGCTGCTCAAACACGACAGGTGTCCATTGGACAACAGAG 349
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LOCUS	BG339057	471 bp mRNA linear EST 27-FB2-2001
DEFINITION	602436882F1 NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4554597 5', mRNA sequence.	RESULT 3
ACCESSION	BG339057	BX283972 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4554597 5'; mRNA sequence.
VERSION	1	LOCUS BX283972 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4554597 5'; mRNA sequence.
KEYWORDS	EST.	DEFINITION BX283972 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4554597 5'; mRNA sequence.
SOURCE	Homo sapiens (human)	ACCESSION BX283972
ORGANISM	Homo sapiens	VERSION BX283972.1 GI:28848426
COMMENT	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	KEYWORDS EST.
REFERENCE	1 (bases 1 to 471) NIH-MGC http://mgc.ncbi.nih.gov/	SOURCE Homo sapiens (human)
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)	ORGANISM Homo sapiens
TITLE	Unpublished (1999)	REFERENCE Authors Raderof, U., Schneider, D., and Korn, B.
JOURNAL	Contact: Robert Strausberg, Ph.D.	TITLE Human UniGeneSet - RZPD3
COMMENT	Email: cgsabs-r@mail.nih.gov	JOURNAL Unpublished (2003)
REFERENCE	Tissue Procurement: NIGC	COMMENT Contact: Ina Rolfs
AUTHORS	CDNA Library Preparation: Ling Hong/Rubin Laboratory	RZPD Deutsches Ressourzzentrum fuer Genomforschung GmbH
TITLE	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LHN)	Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
JOURNAL	DNA Sequencing by: Incyte Genomics, Inc.	RZPD, IMAGP958P11435, RZPD, IMAGP958P11435, RZPD, IMAGP958P11435
COMMENT	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LHN at:	RZPD, IMAGP958P11435, RZPD, IMAGP958P11435, RZPD, IMAGP958P11435
FEATURES	http://Image.lhn.gov	RZPD, IMAGP958P11435, RZPD, IMAGP958P11435, RZPD, IMAGP958P11435
source	Plate: LICM154 row: d column: 22	RZPD Deutsches Ressourzzentrum fuer Genomforschung GmbH
	High quality sequence stop: 470.	Heubnerweg 6, D-14059 Berlin, Germany
	Location/Qualifiers	Tel.: +49 30 32639 101
	1..471	Fax: +49 30 32639 111
	/organism="Homo sapiens"	www.rzpd.de
	/mol_type="mRNA"	This clone is available royalty-free from RZPD, contact RZPD (clone@rzpd.de) for further information.
	/db_xref="taxon:9606"	Location/Qualifiers
	/clone="IMAGE:4554597"	pcMV-M13u, Primer sequence: CGTTGTAACGAGGCCAGT.
	/tissue_type="leionyosarcoma cell line"	1..473 /organism="Homo sapiens"
	/lab_host="DH10B (phage-resistant)"	/mol_type="mRNA"
	/clone_lib="NIH_MGC_46"	/db_xref="taxon:9606"
	EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XbaI sites using the following 5' adaptor: GGACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC	/clone=IMAGE:4554597 1..473 /tissue_type="choriocarcinoma"
		/lab_host="DH10B (phage-resistant)"
		/clone_lib="NIH_MGC_21"
		/note="Organ: placenta; Vector: pOTB7; Site_1: XbaI;"
ORIGIN		

site 2: *Bcori*; cDNA made by oligo-dT priming.  
 Directionally cloned into *Bcori/XbaI* sites using the following 5' adaptor: GGCAGG(G). Size-selected >500bp for average insert size 1.8Kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using SuperScript II RT-PCR Technologies kit (Stratagene).

/lab.host="DH10B (T1 phage-resistant)"  
 /clone.lib="NTH MGC 60"  
 [/note="Organ: Prokaryote; Vector: pDNR-LIB (Clontech);  
 Site 1: SII: (ggccgttcggcc); Site 2: SFII  
 (ggccat tagggcc); Double- and triad adaptors were prepared from  
 cell line RNA. 5' and 3' adaptors were used in cloning as  
 follows: 5' adaptor sequence: 5'-CAGGCCATATGGCC-3', and  
 3' adaptor sequence:  
 5'-ATTCTAGGGCGGCGGACATG-DT(30)BN-3' (where B = A,  
 C, or G and N = A, C, G, or T). Average insert size 1.5  
 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts  
 by PCR. This library was enriched for full-length clones  
 and was constructed by Clontech Laboratories (Palo Alto,  
 CA). Note: this is a NTH MGC library.  
 [

Matches	327;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
y	1	ATGGCGCAGGGATGGTGGATACTCCCGAGGCCAACACGGGGCGGCGCAAGAAG	60						
b	7	ATGGCGCAGGGATGGTGGATACTCCCGAGGCCAACACGGGGCGGCGCAAGAAG	66						
y	61	CGCRTGAAACTGAAAGTGAATSCGATAGCCCTCTGGCCCTGGGATATTGTGGTTGAT	120						
b	67	CGCRTGAAACTGAAAGTGAATSCGATAGCCCTCTGGCCCTGGGATATTGTGGTTGAT	126						
y	121	AACCTGCCATCTGGAGAACCACTATTGATCTTGTAGATGTCAGGTAACCCAG	180						
b	127	AACTTGCCATCTGGAGAACCACTATTGATCTTGTAGATGTCAGGTAACCCAG	186						
y	181	GCGTCCGCPACTTCTGAAAGAGTGTACTCTGGCATGGAGCTCTGTAACCATGCTTTCAC	240						
o	187	GCGTCCGCPACTTCTGAAAGAGTGTACTCTGGCATGGAGCTCTGTAACCATGCTTTCAC	246						
y	241	TTCCCACTGCACTCTCGCTGGCTCAAACAGCAAGGTGTCCATTGGACAACAGAGAG	300						
o	247	TTCCCACTGCACTCTCGCTGGCTCAAACAGCAAGGTGTCCATTGGACAACAGAGAG	306						
y	301	TGGGAATTCCAAAACCTATGGGCACTAG	327						
o	307	TGGGAATTCCAAAACCTATGGGCACTAG	331						

RESULT	4					
LOCUS	BG777485	488 bp	mRNA	linear	EST 15-MAY-2001	
DEFINITION	602664302F1 NIH_MGC_60 Homo sapiens cDNA clone IMAGE:4804661 5', mRNA sequence.					
ACCESSION	BG777485					
VERSION	EST.					
SOURCE	Homo sapiens (human)					
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchoptoglires; Primates; Catarrhini; Hominoidea; Homo.					
REFERENCE	1 (bases 1 to 488)					
AUTHORS	NIH-MGCC					
VERSION	<a href="http://mgc.ncbi.nih.gov/">http://mgc.ncbi.nih.gov/</a>					
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)					
COMMENT	Contact: Robert Strausberg, Ph.D. Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a>					
FEATURES	Source					
	/organism="Homo sapiens" 'mol type="mRNA" 'db Xref="taxon: 9606" 'clone="IMAGE:4804661" 'tissue type="adenocarcinoma"					

FEATURES source	Location/Qualifiers 1. .498 /organism="Pan troglodytes" /mol_type="mRNA" /db_xref="taxon:9598" /clone="12822006_rev_1_C10_r_002.ab1" /sex="male" /tissue type="brain, presumably cortex" /dev stage="adult" /lab_host="Epicurian Coli (TM) XL-10-Gold" /clone lib="Chimpanzee brain library Koos" /note=vector: pIChi; Site 1: SfiI-A; Site 2: SfiI-B; The library was prepared using the SMART cDNA Library construction kit (Clontech), doing only primer extension, but not PCR amplification of the cDNA. The only deviation from the published protocol was that we cloned the cDNA into a plasmid vector."	Fax: 650 473 7760 Email: rbrandenberger@geron.com Insert Length: 509 Std Error: 0.00. Location/Qualifiers 1..509 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="axon:9606" /tissue type="embryonic stem cell, retinoic acid and mitogen-treated HES cell line H7" /clone lib="GRN PRENEU" /note="Oligo dT primed, full-length enriched cDNA library from hES cell line H7 (p29) maintained in feeder-free conditions. Embryooid bodies were generated in the presence of all-trans retinoic acid and mitogens."
FEATURES source	Query Match 100.0%; Score 327; DB 6; Length 498; Best Local Similarity 100.0%; Pred. No. 6.6e-175; Mismatches 0; Indels 0; Gaps 0; Matches 327; Conservative 0; MisMatches 0; Gaps 0;	Query Match 100.0%; Score 327; DB 7; Length 509; Best Local Similarity 100.0%; Pred. No. 6.6e-175; Mismatches 0; Indels 0; Gaps 0; Matches 327; Conservative 0; MisMatches 0; Gaps 0;
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RESULT 7		RESULT 7
LOCUS	BP420485	BP420485
DEFINITION	BP420485 Homo sapiens small intestine Homo sapiens cDNA clone	BP420485 Homo sapiens small intestine Homo sapiens cDNA clone
ACCESSION	BP420485	BP420485
VERSION	BP420485.1	BP420485.1
KEYWORDS	GI:66786738	GI:66786738
SOURCE	EST.	EST.
ORGANISM	Homo sapiens	Homo sapiens
EUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	
REFERENCE	Takeda,J., Jin,L. and Horikawa,Y.	Takeda,J., Jin,L. and Horikawa,Y.
AUTHORS	Unpublished (2005)	Unpublished (2005)
JOURNAL	Journal of Molecular Genetics	Journal of Molecular Genetics
COMMENT	Contact: Yukio Horikawa Laboratory of Molecular and Cellular Institute for Cell, Growth and Differentiation Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan Tel: 81-27-220-8832 Fax: 81-27-220-8839 Email: yhorikawa@showa.gunma-u.ac.jp.	Contact: Yukio Horikawa Laboratory of Molecular and Cellular Genetics Institute for Cell, Growth and Differentiation Showa-machi 3-39-15, Maebashi, Gunma, 371-8512, Japan Tel: 81-27-220-8832 Fax: 81-27-220-8839 Email: yhorikawa@showa.gunma-u.ac.jp.
FEATURES source	Query Match 518 bp mRNA sequence. Best Local Similarity 100.0%; Pred. No. 6.6e-175; Mismatches 0; Indels 0; Gaps 0; Matches 518; Conservative 0; MisMatches 0; Gaps 0;	Query Match 518 bp mRNA sequence. Best Local Similarity 100.0%; Pred. No. 6.6e-175; Mismatches 0; Indels 0; Gaps 0; Matches 518; Conservative 0; MisMatches 0; Gaps 0;
RESULT 6		RESULT 6
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DEFINITION	509 bp mRNA Homo sapiens CDNA 5', mRNA sequence.	509 bp mRNA Homo sapiens CDNA 5', mRNA sequence.
ACCESSION	17000600185586 GRN_PRENEU	17000600185586 GRN_PRENEU
VERSION	CN305892	CN305892
KEYWORDS	CN205892..1 GI:47322306	CN205892..1 GI:47322306
SOURCE	EST.	EST.
ORGANISM	Homo sapiens (human)	Homo sapiens (human)
EUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	EUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	
REFERENCE	Li,Y., Xu,C., Fang,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Lebkowski,J. and Stanton,L.W.	Li,Y., Xu,C., Fang,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J., Lebkowski,J. and Stanton,L.W.
AUTHORS	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation	Transcriptome characterization elucidates signaling networks that control human ES cell growth and differentiation
JOURNAL	Nat. Biotechnol. 22 (6), 707-716 (2004)	Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT	Contact: Brandenberger R Regenerative Medicine Geron Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658	Contact: Brandenberger R Regenerative Medicine Geron Corporation 230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658

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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="HB03775r"
/tissue type="small intestine"
/clone_lib="Homo sapiens small intestine"

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Oy	61 CGCTTGAATGAAAGTGAATGAGTACCCCTGGGCTGGATAATGGGTGAT 74 CCCTTGAGTGAATGAAAGTGGATGGATGGCTGGGATATGGTTGAT	327	0;	518;
Db	121 AACTRGCCATCTGCAGAACCATATTATGGATCTTGCATAGAATGTCAGCTAACAG 134 AACTGTCCTACTCTGAGAGTGTACTCTGAGATGGCTGGGATGGCTGGGATATGGTTGAT	327	0;	518;
Qy	181 GGTCCCTACTCTGAGAGTGTACTCTGAGATGGCTGGGAGTGTGTAACCAGCTTAC 194 GCGTCCCTACTCTGAGAGTGTACTCTGAGATGGCTGGGAGTGTGTAACCAGCTTAC	327	0;	518;
Db	241 TTCCACTGCACTCTCTGGCTCAAACACGACAGCTGCTCCATTGGACAAACGAGAG 254 TTCCACTGCACTCTCTGGCTCAAACACGACAGCTGCTCCATTGGACAAACGAGAG	327	0;	518;
Qy	301 TGGGAATTCCTAAAAGTATGGCCACTAG 314 TGGGAATTCCTAAAAGTATGGCCACTAG	327	0;	518;
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/mol type="mRNA"
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**ORIGIN**

Query	Match	Score	DB	Length
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Db	61 CGCTTGAATGAAAGTGAATGAGTACCCCTGGGCTGGATAATGGGTGAT 81 CGCTTGAATGAAAGTGAATGAGTACCCCTGGGCTGGATAATGGGTGAT	327	0;	522;
Qy	121 AACCTGCCATCTGCAGAACCATATTATGGATCTTGCATAGAATGTCAGCTAACAG 141 AACCTGCCATCTGCAGAACCATATTATGGATCTTGCATAGAATGTCAGCTAACAG	327	0;	522;
Db	181 GGTCCCTACTCTGAGAGTGTACTCTGAGATGGCTGGGAGTGTGTAACCAGCTTAC 201 GGTCCCTACTCTGAGAGTGTACTCTGAGATGGCTGGGAGTGTGTAACCAGCTTAC	327	0;	522;
Qy	241 TTCCACTGCACTCTCTGGCTCAAACACGACAGCTGCTCCATTGGACAAACGAGAG 261 TTCCACTGCACTCTCTGGCTCAAACACGACAGCTGCTCCATTGGACAAACGAGAG	327	0;	522;
Db	301 TGGGAATTCCTAAAAGTATGGCCACTAG 321 TGGGAATTCCTAAAAGTATGGCCACTAG	327	0;	522;

**RESULT** 8  
**AL711573**  
**LOCUS** AL711573  
**DEFINITION** DKFP68610483 r1\_686 (synonym: h1cc3) Homo sapiens cDNA clone  
**ACCESSION** DKFP68610483\_5  
**VERSION** AL711573  
**KEYWORDS** EST  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**MATERIAL** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
**HOMINIDAE** Mammalia; Eutheria; Buarchoontogires; Primates; Catarrhini;

**REFERENCE** 1 (bases 1 to 522)  
**AUTHORS** Koehler, K., Beyer, A., Newes, W., Weil, B. and Wiemann, S.  
**TITLE** EST (Koehler, K., Beyer, A., Newes, W., Weil, B. and Wiemann, S.)  
**JOURNAL** Unpublished (1999)  
**COMMENT** Contact : MIPS  
**MIPS** Ingolstaedter Landstr. 1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;  
sequenced by BMFZ (Biomedical Research Center at the Charite, Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.  
No s1 sequence available.

This clone (DKFP68610483) is available at the RZPD in Berlin-Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.  
Please contact the RZPD: Resourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

**FEATURES**  
**Source**  
1. 522  
/organism="Homo sapiens"  
/mol type="mRNA"  
/db\_xref="taxon:9606"  
/tissue type="leiomyosarcoma cell line"  
/db\_ho="DR10B (phage-resistant)"  
/clone lib="NINH MG C 46"  
/note="Organ: uTeru; Vector: pOTB7; Site\_1: XhoI; Site\_2:

**RESULT** 9  
**BG337472**  
**LOCUS** BG337472 NIH\_MGC\_46 Homo sapiens mRNA  
**DEFINITION** mRNA sequence.  
**ACCESSION** BG337472  
**VERSION** BG337472.1  
**KEYWORDS** EST  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
**MATERIAL** Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Buarchoontogires; Primates; Catarrhini;  
**HOMINIDAE** Hominidae; Homo.  
**REFERENCE** 1 (bases 1 to 525)  
**AUTHORS** NIH-MGC http://mgc.ncbi.nlm.nih.gov/  
**TITLE** Unpublished (1999)  
**JOURNAL** National Institutes of Health, Mammalian Gene Collection (MGC)  
**COMMENT** Contact : Robert Straubberg, Ph.D.  
Email: cgaps-r@mail.nih.gov  
**Tissue** Procurement: ARCC  
**CDNA Library Preparation: Ling Hong/Rubin Laboratory**  
**CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LHN)**  
**DNA Sequencing by: Incyte Genomics Inc.**  
**Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LHN at:**  
http://image.lhn1.gov  
**Plate: LLCM1250**: row: e column: 01  
High quality sequence step: 525.  
**Location/Qualifiers**  
1. 525  
/organism="Homo sapiens"  
/mol type="mRNA"  
/db\_xref="taxon:9606"  
/tissue type="leiomyosarcoma cell line"  
/db\_ho="DR10B (phage-resistant)"  
/clone lib="NINH MG C 46"  
/note="Organ: uTeru; Vector: pOTB7; Site\_1: XhoI; Site\_2:

ECORI: cDNA made by oligo-dT priming. Directionally cloned into ECO RI/Xba I sites using the following 5' adapter: GGCAAG(G)500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match	100.0%	Score 327; DB 2; Length 525;
Best Local Similarity	100.0%	Pred. No. 6.6e-15; Indels 0; Gaps 0;
Matches	327;	Conservative 0; Mismatches 0;
Qy	1	ATGGGGCACCGGATGGATGTGGATAACCCAGCGGCCAACACGGGGAAAGAG 60
Db	7	ATGGGGCACCGGATGGATGTGGATAACCCAGCGGCCAACACGGGGAAAGAG 66
Qy	61	CGCTTGAACTGAAAAGGTGAAATCAGTGCCTCTGGGATATTGGTTGAT 120
Db	67	CGCTTGAACTGAAAAGGTGAAATCAGTGCCTCTGGGCTGGATAATTGGTTGAT 126
Qy	121	AACCTGCCATCTGGAGAACCATTAATGGATCTTGGATAGAATGTCAAGCTAACCAAG 180
Db	127	AACCTGCCATCTGGAGAACCATTAATGGATCTTGGATAGAATGTCAAGCTAACCAAG 186
Qy	181	GCGTCGGTACTCTGAGAAGTGTACTGTGCAATGGGAGCTGTAAACATGTTAAC 240
Db	187	GCGTCGGTACTCTGAGAAGTGTACTGTGCAATGGGAGCTGTAAACATGTTAAC 246
Qy	241	TTCGACTGATCTCNGCTGCTCAAACACGACAGGTGTCCATTGACAACAGAG 300
Db	247	TTCGACTGATCTCNGCTGCTCAAACACGACAGGTGTCCATTGACAACAGAG 306
Qy	301	TGGGAATCCAAACTGGCACTAG 327
Db	307	TGGGAATCCAAACTGGCACTAG 333

RESULT 10  
BM715215 LOCUS BM715215 527 bp mRNA linear EST 28-FBB-2002 DEFINITION UI-E-CU1-af1-h-19-0-UI.r2 UI-E-CU1 Homo sapiens cDNA clone UI-E-CU1-af1-h-19-0-UI 5', mRNA sequence.

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.  
1 (bases 1 to 527)

Bonaldo, M.F.; Lennon, G. and Soares, M.B.  
Normalization and subtraction: two approaches to facilitate gene discovery

Genome Res. 6 (9), 791-806 (1996)

888548

Email: bento\_soares@uiowa.edu

Contact: Soares, MB

Coordinated Laboratory for Computational Genomics

University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Tissue Procurement: Dr. Greg Hageman  
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).  
Seq primer: M13 Reverse.

FEATURES  
COMMENT  
JOURNAL  
PUBLMED  
REFERENCE  
AUTHORS  
TITLE  
COMMENT  
LOCATION/QUALIFIERS

## source

1. .527 /organism="Homo sapiens"	/mol_type="mRNA"	/db_xref="Taxon:9606"	/clone="UI-E-CU1-af1-h-19-0-UI"	/tissue_type="human retina"	/dev_stage="adult"	/lab_host="IDH108 (Life Technologies)"	/clone_id="UI-E-CU1"	/note="Organ: eye; Vector: pPT73-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Not I; UI-E-CU1 is a normalized cDNA library containing the following tissue(s): retina. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pPT73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (DR)18 tail. The sequence tag for this library is CCGCG. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI)."
ORIGIN	Query Match	Score 327; DB 3; Length 527;	Best Local Similarity	100.0%;	Pred. No. 6.6e-175;	Indels 0;	Gaps 0;	Matches 327; Conservative 0; Mismatches 0;
Qy	1	ATGGGGCACCGGATGGATAACCCAGCGGCCAACACGGGGAAAGAG 60	Db	4	ATGGGGCACCGGATGGATAACCCAGCGGCCAACACGGGGAAAGAG 60	Qy	1	ATGGGGCACCGGATGGATAACCCAGCGGCCAACACGGGGAAAGAG 60
Qy	61	CGCTTGAACTGAAAAGGTGAAATCAGTGCCTCTGGGATATTGGTTGAT 120	Db	64	CGCTTGAACTGAAAAGGTGAAATCAGTGCCTCTGGGATATTGGTTGAT 120	Qy	61	CGCTTGAACTGAAAAGGTGAAATCAGTGCCTCTGGGATATTGGTTGAT 120
Qy	121	AACCTGCCATCTGGAGAACCATTAATGGATCTTGGATAGAATGTCAAGCTAACCAAG 180	Db	64	CGCTTGAACTGAAAAGGTGAAATCAGTGCCTCTGGGATATTGGTTGAT 123	Qy	62	CGCTTGAACTGAAAAGGTGAAATCAGTGCCTCTGGGATATTGGTTGAT 123
Qy	181	GCGTCGGTACTCTGAGAAGTGTACTGTGCAATGGGAGCTGTAAACATGTTAAC 240	Db	124	AACCTGCCATCTGGAGAACCATTAATGGATCTTGGATATTGGTTGAT 183	Qy	181	GCGTCGGTACTCTGAGAAGTGTACTGTGCAATGGGAGCTGTAAACATGTTAAC 240
Db	187	GCGTCGGTACTCTGAGAAGTGTACTGTGCAATGGGAGCTGTAAACATGTTAAC 246	Db	184	GCGTCGGTACTCTGAGAAGTGTACTGTGCAATGGGAGCTGTAAACATGTTAAC 243	Qy	181	GCGTCGGTACTCTGAGAAGTGTACTGTGCAATGGGAGCTGTAAACATGTTAAC 240
Qy	241	TTCGACTGATCTCNGCTGCTCAAACACGACAGGTGTCCATTGACAACAGAG 300	Db	241	TTCGACTGATCTCNGCTGCTCAAACACGACAGGTGTCCATTGACAACAGAG 300	Qy	181	GCGTCGGTACTCTGAGAAGTGTACTGTGCAATGGGAGCTGTAAACATGTTAAC 240
Db	247	TTCGACTGATCTCNGCTGCTCAAACACGACAGGTGTCCATTGACAACAGAG 306	Db	244	TTCGACTGATCTCNGCTGCTCAAACACGACAGGTGTCCATTGACAACAGAG 303	Qy	181	GCGTCGGTACTCTGAGAAGTGTACTGTGCAATGGGAGCTGTAAACATGTTAAC 180
Qy	301	TGGGAATCCAAACTGGCACTAG 327	Db	304	TGGGAATCCAAACTGGCACTAG 330	Qy	301	TGGGAATCCAAACTGGCACTAG 327.
Db	307	TGGGAATCCAAACTGGCACTAG 333	Db			RESULT 11	BU932751	BU932751
LOCUS	BU932751	527 bp mRNA linear EST 18-OCT-2002	LOCUS	BU932751	527 bp mRNA linear EST 18-OCT-2002			
DEFINITION	UI-E-CU1-af1-h-19-0-UI.r2	UI-E-CU1 Homo sapiens cDNA clone	DEFINITION	AGENCOURT 10473929 NIH_MGC 127 Homo sapiens cDNA clone	DEFINITION	IMAGE:6673337 5', mRNA sequence.		
ACCESSION	BU715215	BU715215.1 GI:19028473	ACCESSION	BU932751	BU932751	ACCESSION	BU932751.1 GI:24121570	
VERSION			VERSION			VERSION		
KEYWORDS			KEYWORDS			KEYWORDS		
SOURCE	Homo sapiens (human)		SOURCE	Homo sapiens (human)		SOURCE	Homo sapiens (human)	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.		ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.		ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo.	
REFERENCE			REFERENCE			REFERENCE		
AUTHORS			AUTHORS			AUTHORS		
TITLE			TITLE			TITLE		
JOURNAL			JOURNAL			JOURNAL		
PUBLMED			PUBLMED			PUBLMED		
COMMENT			COMMENT			COMMENT		

Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: NCI  
cDNA Library Preparation: Michael Brownstein Laboratory  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
DNA Distribution by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov

Plate: LNCM2955 row: e column: 17  
Location/Qualifiers  
1..527  
High quality sequence stop: 98.

FEATURES  
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/clone="IMAGE:6673337"  
/tissue\_type="mixed (pool of 40 RNAs)"  
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/clone\_lib="NIH MGC 127"  
/notes="Vector: PDR-LIB; Site\_1: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.3%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:  
5'-AAGCTTACGCTTATCAAGCAGAATGCTGGCGATACGGCCGG-3'  
5'-ATTCTAGAGGCCATGGATGGTGGATACCCGAGGGGCCAACAGGGCAAGAAG 60  
enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 1-2 kb size fraction (other fractions present in NIH MGC NIH MGC 128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH\_MGC Library."

ORIGIN

Query Match	Score	Length	DB	Best Local Similarity	Pred.	No.	Mismatches	Indels	Gaps	0;
1 ATGGCCCAAGCGATGGATGGTGGATACCCGAGGGGCCAACAGGGCAAGAAG 60	100.0%	527	Db	327	100.0%	6..6..175	0	0	0	;
24 ATGGCCCAAGCGATGGATGGTGGATACCCGAGGGGCCAACAGGGCAAGAAG 83			Db	327	100.0%	6..6..175	0	0	0	;
Qy 1 CGCTTAAAGTAAAAGTGGATGGTAGCCATTGGCTGGGATATTGGTTGAT 120	Qy	100.0%	Db	327	100.0%	6..6..175	0	0	0	;
84 CGCTTAAAGTAAAAGTGGATGGTAGCCATTGGCTGGGATATTGGTTGAT 143	Db				Conservative	0;	Mismatches	0;	Indels	0;
Qy 121 AACTGTTCCCTACTTCAGAAGTGTACTGTCTCATGGGAGCTGTGAACTAACAG 180	Qy	100.0%	Db	327	100.0%	6..6..175	0	0	0	;
Db 144 AACTGTTCCCTACTTCAGAAGTGTACTGTCTCATGGGAGCTGTGAACTAACAG 203	Db				Conservative	0;	Mismatches	0;	Indels	0;
Qy 181 GCGTCCCTACTTCAGAAGTGTACTGTCTCATGGGAGCTGTGAACTAACAG 240	Qy	100.0%	Db	327	100.0%	6..6..175	0	0	0	;
Db 204 GCGTCCCTACTTCAGAAGTGTACTGTCTCATGGGAGCTGTGAACTAACAG 263	Db				Conservative	0;	Mismatches	0;	Indels	0;
Qy 241 TTCCACTGCACTCTCGCTGGCTCAAACAGACAGGTGTCTCATGGGAG 300	Qy	100.0%	Db	327	100.0%	6..6..175	0	0	0	;
Db 264 TTCCACTGCACTCTCGCTGGCTCAAACAGACAGGTGTCTCATGGGAG 323	Db				Conservative	0;	Mismatches	0;	Indels	0;
Qy 301 TGGGAATTCAAAAGTGGCACTAG 327	Qy	100.0%	Db	327	100.0%	6..6..175	0	0	0	;
Db 324 TGGGAATTCAAAAGTGGCACTAG 350	Db				Conservative	0;	Mismatches	0;	Indels	0;

RESULT 12  
CB999822 LOCUS  
DEFINITION AGENCOURT 13645988 NIH MGC 186 Homo sapiens cDNA clone IMAGE:30322649 5', mRNA sequence.  
ACCESSION CB999822

VERSTON EST.  
KEYWORD Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo  
1 (bases 1 to 527)  
NIH-MGC http://mgc.ncbi.nlm.nih.gov/

REFERENCE 1  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution: Agencourt Bioscience Corporation  
http://image.llnl.gov  
plate: NDCM123 row: P column: 18  
High quality sequence stop: 518.  
Location/Qualifiers  
1..527  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6673337"  
/tissue\_type="mixed (pool of 40 RNAs)"  
/lab\_host="DH10B (T1-phage-resistant)"  
/clone\_lib="NIH MGC 127"  
/notes="Vector: PDR-LIB; Site\_1: SfiI (ggccattatggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.3%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:  
5'-AAGCTTACGCTTATCAAGCAGAATGCTGGCGATACGGCCGG-3'  
5'-ATTCTAGAGGCCATGGTGGATACCCGAGGGGCCAACAGGGCAAGAAG 60  
enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 1-2 kb size fraction (other fractions present in NIH MGC NIH MGC 128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH\_MGC Library."

FEATURES  
source  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
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/lab\_host="DH10B (T1-phage-resistant)"  
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ORIGIN

Query Match Score 327; DB 6; Length 527;  
Best Local Similarity 100.0%; Pred. No. 6..6..175;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCCCAAGCGATGGATGGTGGATACCCGAGGGGCCAACAGGGCAAGAAG 60  
24 ATGGCCCAAGCGATGGATGGTGGATACCCGAGGGGCCAACAGGGCAAGAAG 83

ORIGIN

Query Match Score 327; DB 6; Length 527;  
Best Local Similarity 100.0%; Pred. No. 6..6..175;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCCCAAGCGATGGATGGTGGATACCCGAGGGGCCAACAGGGCAAGAAG 60  
84 CGCTTAAAGTAAAAGTGGATGGTAGCTGGCTGGCATATTGTGGTTGAT 143

Db

Qy 121 AACTGTTCCCTACTTCAGAAGTGTACTGTCTCATGGGAGCTGTGAACTAACAG 180  
Db 144 AACTGTTCCCTACTTCAGAAGTGTACTGTCTCATGGGAGCTGTGAACTAACAG 203

Qy 181 GCGTCCCTACTTCAGAAGTGTACTGTCTCATGGGAGCTGTGAACTAACAG 240  
Db

Qy 241 TTCCACTGCACTCTCGCTGGCTCAAACAGACAGGTGTCTCATGGGAG 300  
Db 264 TTCCACTGCACTCTCGCTGGCTCAAACAGACAGGTGTCTCATGGGAG 323

Qy 301 TGGGAATTCAAAAGTGGCACTAG 327  
Db 324 TGGGAATTCAAAAGTGGCACTAG 350

RESULT 12  
LOCUS  
DEFINITION AGENCOURT 13645988 NIH MGC 186 Homo sapiens cDNA clone IMAGE:30322649 5', mRNA sequence.  
ACCESSION CB999822

VERSTON EST.  
KEYWORD Homo sapiens (human)  
ORGANISM Homo sapiens  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Homo  
1 (bases 1 to 527)  
NIH-MGC http://mgc.ncbi.nlm.nih.gov/

REFERENCE 1  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits  
cDNA Library Preparation: CLONTECH Laboratories, Inc.  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution: Agencourt Bioscience Corporation  
http://image.llnl.gov  
plate: NDCM123 row: P column: 18  
High quality sequence stop: 518.  
Location/Qualifiers  
1..527  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
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/clone="IMAGE:30322649"  
/lab\_host="DH10B (T1-phage-resistant)"  
/clone\_lib="NIH MGC 186"  
/notes="Vector: pDNR-LIB; Site\_1: SfiI (ggccgttcggcc); Library is oligo-dt primed and directionally cloned. CDNA was prepared from a pooled samples of tissues from Skin, meninges, duramater, pia matter and choroid plexus, and 3' adaptors were used in cloning as follows: 5', adaptor sequence: 5'-CACGGCCATTATGGCC-3', and 3' adaptor sequence: 5'-ATTCTAGAGGCCATGGTGGATACGGCGT-3' (30) BN-3, (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library"

FEATURES  
source  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
/clone="IMAGE:30322649"  
/lab\_host="DH10B (T1-phage-resistant)"  
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/notes="Vector: pDNR-LIB; Site\_1: SfiI (ggccgttcggcc); Library is oligo-dt primed and directionally cloned. CDNA was prepared from a pooled samples of tissues from Skin, meninges, duramater, pia matter and choroid plexus, and 3' adaptors were used in cloning as follows: 5', adaptor sequence: 5'-CACGGCCATTATGGCC-3', and 3' adaptor sequence: 5'-ATTCTAGAGGCCATGGTGGATACGGCGT-3' (30) BN-3, (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.47 kb (range 0.50-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC Library"

ORIGIN

Query Match Score 327; DB 6; Length 527;  
Best Local Similarity 100.0%; Pred. No. 6..6..175;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCCCAAGCGATGGATGGTGGATACCCGAGGGGCCAACAGGGCAAGAAG 60  
84 CGCTTAAAGTAAAAGTGGATGGTAGCTGGCTGGCATATTGTGGTTGAT 143

Db

Qy 121 AACTGTTCCCTACTTCAGAAGTGTACTGTCTCATGGGAGCTGTGAACTAACAG 180  
Db 144 AACTGTTCCCTACTTCAGAAGTGTACTGTCTCATGGGAGCTGTGAACTAACAG 203

Qy 181 GCGTCCCTACTTCAGAAGTGTACTGTCTCATGGGAGCTGTGAACTAACAG 240  
Db

Qy 241 TTCCACTGCACTCTCGCTGGCTCAAACAGACAGGTGTCTCATGGGAG 300  
Db 264 TTCCACTGCACTCTCGCTGGCTCAAACAGACAGGTGTCTCATGGGAG 323

Qy 301 TGGGAATTCAAAAGTGGCACTAG 327  
Db 324 TGGGAATTCAAAAGTGGCACTAG 350

RESULT 12  
LOCUS  
DEFINITION AGENCOURT 13645988 NIH MGC 186 Homo sapiens cDNA clone IMAGE:30322649 5', mRNA sequence.  
ACCESSION CB999822

RESULT	13	BM757406	BM757406	K-EST0036388	S1SN5 Homo sapiens	529 bp	mRNA	linear	EST 04-MAR-2002	
LOCUS				sequence.						
DEFINITION				BM757406	S1SN5 Homo sapiens	CDNA clone S1SN5-29-H12 5', mRNA				
ACCESSION				BM757406						
VERSION				BM757406..1	GI:19087021					
SOURCE				Homo sapiens (human)						
ORGANISM				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo						
REFERENCE				1. (bases 1 to 529)						
AUTHORS				Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.						
TITLE				21C Frontier Korean EST Project 2001						
JOURNAL				Unpublished						
COMMENT				Contact: Kim YS						
FEATURES	source			Genome Research Center						
				52, Baeun-dong Yuseong-gu, Daejeon 305-333, South Korea						
				Te: +82-42-860-4470						
				Fax: +82-42-860-4409						
				Email: yongsung@mail.kribb.re.kr						
				Plate: 29 row: H column: 12						
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				/cell_line="SNU-5"						
				/lab_host="TOP10F"						
				/clone_id="S1SN5"						
				/note="Organ: Stomach; Vector: pCNS; Site 1: ECORI; Site 2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tobacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECO RI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of ECO RI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."						
				ORIGIN						
				Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 327; Conservation 0;	Score 327; DB 3; Length 529;					
				Pred. No. 6 6e-175; N mismatches 0;	Pred. No. 6 6e-175; N mismatches 0;					
				Indels 0; Gaps 0;	Indels 0; Gaps 0;					
Qy	1	ATGGGGCACGCGATGGATAACCCGAGGCCACCAACAGGGGGAAAGAG	60							
Db	33	ATGGGGCACGCGATGGATAACCCGACGCCCTGTGGATATGTGGTGTATGTGCTGTGAT	92							
Qy	61	CGCTTTGAACTGAAAGTGAATGGAATGCAATTATGATGTCATAGTCAAGTCAACCGAG	120							
Db	93	CGCTTTGAACTGAAAGTGAATGCAATTATGATGTCATAGTCAAGTCAACCGAG	180							
				Query Match Score 100.0%; Best Local Similarity 100.0%; Pred. No. 6 6e-175; Length 531;	Score 327; DB 6; Length 531;					

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGGCGGAGCCATGGATGGATAACCCGAGCGGCCAACAGGGCGGGCAAGAA 60

Db 23 ATGGCGGAGCCATGGATGGATAACCCGAGCGGCCAACAGGGCGGGCAAGAAG 82

Oy 61 CGCTTGAAGTCAAAAGTGGATGCGTAGCGCTGGGATATGGCTGTGAT 120

Db 83 CGCTTGAAGTCAAAAGTGGATGCGTAGCGCTGGGCTGGGATATGGCTGTGAT 142

Oy 121 AACTGTCCCATGAGAACATATGGATCTTGCTAGAATGTCAGCTAACAG 180

Db 143 AACTGTCCCATGAGAACATATGGATCTTGCTAGAATGTCAGCTAACAG 202

Oy 181 GGTCCTACTCAGAGAGTGTGACTGTGGATGGAGTGTGAAATGCTTTAC 240

Db 203 GGTCCTACTCAGAGAGTGTGACTGTGGATGGAGTGTGAAATGCTTTAC 262

OY 241 TTCCACTGCATCTCTGGCTCAAACACGACAGCTGTCATGGACAACAGAGAG 300

Db 263 TTCCACTGCATCTCTGGCTCAAACACGACAGCTGTCATGGACAACAGAGAG 322

Oy 301 TGGGAATTCCAAAAGTATGGGCACTAG 327

Db 323 TGGGAATTCCAAAAGTATGGGCACTAG 349

RESULT 16

BU729963/c

LOCUS 533 bp mRNA linear EST 09-OCT-2002

DEFINITION UI-E-CK1-af1-h-19-0-UI s1 UI-E-CK1 Homo sapiens cDNA clone.

VERSION BU729963.1 GI: 23653376

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

REFERENCE 1 (bases 1 to 533).

AUTHORS Bonaldo, M.F., Lennon, G. and Soares, M.B.

TITLE Normalization and subtraction: two approaches to facilitate gene discovery.

JOURNAL Genome Res. 6 (9), 791-806 (1996)

PUBMED 8889548

COMMENT Contact: Soares, MB  
Coordinated Laboratory for Computational Genomics  
University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565  
Email: bento-soares@uiowa.edu

Tissue procurement: Dr. Gregg Hageman  
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Researchers may obtain clones from Research Genetics ([www.resgen.com](http://www.resgen.com)).  
Seq Primer: M13 FORWARD

POLYA=Yes

FEATURES Location/Qualifiers

source 1..533

/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="UI-E-CK1-af1-h-19-0-UI"  
/tissue\_type="Retina Foveal and Macular"  
/dev\_stage="adult"  
/lab\_host="DHIOB (Life Technologies) (T1 phage resistant)"  
/clone\_lib="UI-E-CK1"  
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site\_1: EcoRI I; Site\_2: Not I;"

UI-E-CK1 is a normalized cDNA library containing the following tissue(s): Retina Foveal and Macular. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adapter, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GRCC. This library was created for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).

TAG LIB=UI-E-CK1

TAG SEQ=GTCC"

## ORIGIN

Query	Match	100.0%	Score 327;	DB 5;	Length 533;
	Best Local Similarity	100.0%	Pred. No. 6..175;		
	Matches	327;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1 ATGGCGGAGGGATGGATGTGGATAACCCGAGCGGCCACCAAGCGGCCAGCAAGAAG 60				
Db	518 ATGGCGGAGGGATGGATGTGGATAACCCGAGCGGCCACCAAGCGGCCAGCAAGAAG 459				
Qy	61 CGCTTGAAGTGAAGTGAATTCAGTAGCCCTGCGGATATTGGTGTGAT 120				
Db	458 CGCTTGAAGTGAAGTGAATTCAGTAGCCCTGCGGATATTGGTGTGAT 399				
Qy	121 AACGTGCGCATCTGGAGAACATTGGATCTTGATAGATGTCAAGCTAACAG 180				
Db	398 AACGTGCGCATCTGGAGAACATTGGATCTTGATAGATGTCAAGCTAACAG 339				
Qy	181 GCGTCGGCTACTCTGGAGGTGTACTGTGGAGTCTGTAACCATGTTTCAC 240				
Db	338 GCGTCGGCTACTCTGGAGGTGTACTGTGGAGTCTGTAACCATGTTTCAC 279				
Qy	241 TTCACTGCATCTGGCTGCTCAAACACGAGGTGTACTGTGGAGTCTGTAACCATGTTTCAC 300				
Db	278 TTCACTGCATCTGGCTGCTCAAACACGAGGTGTACTGTGGAGTCTGTAACCATGTTTCAC 299				
Qy	301 TGGGATTCCAAAAGTATGGGCACTAG 327				
Db	218 TGGGATTCCAAAAGTATGGGCACTAG 192				

RESULT 16

BG478622

LOCUS 537 bp mRNA linear EST 21-MAR-2001

DEFINITION 602525509F1 NIH\_MGC\_20 Homo sapiens cDNA clone IMAGE:4613619 5', mRNA sequence.

ACCESSION BG478622

VERSION BG478622.1 GI:13410901

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.

Hominidae; Homo.

Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgsabs@mail.nih.gov

Tissue Procurement: ATCC/DCTD/BTP

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at:

http://image.llnl.gov  
 Plate: ILCM1414 row: b column: 04  
 High quality sequence stop: 534.  
 Location/Qualifiers  
   1. .537  
     Source  
       /mol\_type="mRNA"  
       /db\_xref="taxon:9606"  
       /clone="IMAGE:4641619"  
       /tissue\_type="melanotic melanoma"  
       /lab\_host="DH10B (phage-resistant)"  
       /clone\_id="b- NIH MGC 20"  
       /NOTE="Organ: skin; Vector: pORTB7; Site\_1: XbaI; Site\_2:  
         ECORI; cDNA made by oligo-dT priming. Directionally  
         cloned into EcoRI/XbaI sites using the following 5'  
         adaptor: GGCAGAG (G). Size-selected >500bp for average  
         insert size 1.8kb. Library constructed by Ling Hong in  
         the laboratory of Gerald M. Rubin (University of  
         California, Berkeley) using ZAP-cDNA synthesis kit  
         (Stratagene) and Superscript II RT (Life Technologies)."  
  
 ORIGIN  
  

	Query Match	Match
Qy	100.0%	Score 327; DB 2; Length 537;
Best Local Similarity	100.0%	Pred. No. 6.6e-175;
Matches	327;	Mismatches 0; Indels 0; Gaps 0;
Qy	1 ATGGCCGCAAGGATGGATGTGGATACCCGAGGGCACCACAGGGCGGGAAAGAG 60	
Db	19 ATGGCCGCAAGGATGGATGTGGATACCCGAGGGCACCACAGGGCGGGAAAGAG 78	
Qy	61 CGCTTGAAGTAAAGTGAATGGAGTGGCTCTGGCATGGATATTGGTGTAT 120	
Db	79 CGCTTGAAGTAAAGTGAATGGAGTGGCTCTGGCATGGATATTGGTGTAT 138	
Qy	121 AACTGTGCCATTGCGGAAACACATTATGGATCTTCATAGAATGTCAAGTAACCG 180	
Db	139 AACTGTGCCATTGCGGAAACACATTATGGATCTTCATAGAATGTCAAGTAACCG 198	
Qy	181 GGTCTCCCTACTCTGAGAGTGTACTGTCATGGGACTCTGTAAACATGGCTTTCAC 240	
Db	199 GGTCTCCCTACTCTGAGAGTGTACTGTCATGGGACTCTGTAAACATGGCTTTCAC 258	
Qy	241 TTCCACTGCACTCTCGCTGGTCAAAACAGAACAGTGTTGCAATTGGACAAAGAGAG 300	
Db	259 TTCCACTGCACTCTCGCTGGTCAAAACAGAACAGTGTTGCAATTGGACAAAGAGAG 318	
Qy	301 TGGGAATTCCAAAAGTATGGGACTAG 327	
Db	319 TGGGAATTCCAAAAGTATGGGACTAG 345	

  
 RESULT 17  
 BU941262 LOCUS DEFINITION AGENCOURT 10512526 NIH MGC 127 Homo sapiens mRNA clone EST 18-OCT-2002  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo  
 1 (bases 1 to 545)  
 REFERENCE NIH-NCI http://mgc.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Comment Contact: Robert Straussberg, Ph.D.  
 Email: cspbbs-r@mail.nih.gov  
 Tissue Procurement: NCI  
 CDNA Library Preparation: Michael Brownstein Laboratory  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:  
<http://image.llnl.gov>  
 Plate: LLNL3023 row: h column: 20  
 High quality sequence stop: 522.

FEATURES	source
	Location/Qualifiers
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/mol_type="mRNA"	
/db_xref="taxon:9606"	
/clone=IMAGE:6713348"	
/tissue_type="mixed (pool of 40 RNAs)"	
/lab_host="DH10B (MGC 127"	
/clone_lib="NIH MGC 127"	
/note="Vector: pDR-LIB; Site_1: SfiI (ggccattatggcc); Site_2: Sf <sub>1</sub> I (ggccgcctcgcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladd	
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%.	
5, and 3', adaptors were used in cloning as follows:	
5'-AAGCTTGGTATCAAGCAGTCATTAGGGCCGG-3' and	
5'-ATTCTAGGGCGAGGGCCGAGCGGCACTG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 1-2 size fraction (other fractions present in NIH MGC 126, NIH MGC 128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGG_Library."	
	ORIGIN



Db	313	TGGAAATCCAAAAGTATGGCACTAG	339
RESULT	20		
LOCUS	AV716338	548 bp mRNA	EST 11-OCT-2000
DEFINITION	AV716338 DCB Homo sapiens cDNA clone DCBAFE06 5'	mRNA sequence.	
ACCESSION	AV716338		
VERSION	AV716338.1	GI:10797855	
KEYWORDS	Homo sapiens (human)		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 548)		
AUTHORS	Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,J., Gao,G., Xiao,H., Li,N., Qian,B., Geo,X., Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Cheng,Z., and Han,Z.		
TITLE	Homo sapiens cDNA DCB clones		
JOURNAL	Unpublished (2000)		
COMMENT	Contact: Zeguang Han Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919 (ext.45) Fax: 86-21-50801922 Email: hanzg@chgc.sh.cn		
FEATURES	source		
		/organism="Homo sapiens" (/mol_type="mRNA")	
		/db_xref="taxon:9606"	
		/clone="IMAGE:6495192"	
		/tissue-type="mixed (pool of 40 RNAs)"	
		/lab_host="DH10B (11-phage-resistant)"	
		/clone_lib="NIH MGC 142"	
		/note="Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site 2: SfiI (ggccgcgtcgcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2+, blood - 33.4%, brain 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%." 5, and 3, adaptors were used in cloning as follows: 5'-ATTCTAGGGCGAGGCGGCCATAGCT-dt (30) NN 3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH MGC 141). Library created in the laboratory of M. Brownstein (NIH, NIH). Note: this is a NIH_MGC Library."	
ORIGIN			
FEATURES	source		
		Query Match Score 327; DB 1; Length 548;	
		Best Local Similarity 100.0%; Pred. No. 6.6e-175; Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1	ATGCCGGAGCGGTGGATGGATACCCGGAGCGCACACAGCGGCCGAG 60	
Db	37	ATGCCGGAGCGGTGGATGGATACCCGGAGCGCACACAGCGGCCGAG 96	
Qy	61	CCTTTGAAGTAAAAAGTGAATGCAATGACCCCTGGATATGTGGTGT 120	
Db	97	CGTTTGAGTGAAAAGTGAATGCAATGACCCCTGGATATGTGGTGT 156	
Qy	121	AACCTGTGCCATCTCGAGAACCATTAAGTCAATGCTTGTCAACCTGCT 180	
Db	157	AACCTGTGCCATCTCGAGAACCATTAAGTCAATGCTTGTCAACCTGCT 216	
Qy	181	GCGTCGTCACTTAGAAGGTGACTGTGCACTGGGCTGTAACTGCTTCA 240	
Db	217	GGCTCGCTGTCACTTCGCTGCTCAAACAGCAAGGTGTCACTGGGCTGT 276	
Qy	241	TTCCTACTGTCTCTCGTGTCAAAACAGCAAGGTGTCACTGGGCTGT 300	
Db	277	TTCCTACTGTCTCTCGTGTCAAAACAGCAAGGTGTCACTGGGCTGT 336	
Qy	301	TGGAAATTCCAAAAGTATGGCACTAG 327	
Db	337	TGGAAATTCCAAAACATGGCACTAG 363	
Qy	381	GGCTCCGCTACTTCGATCTGCACTGGGAGTCGATGGTCAACATGCTTTCAC 240	
Db	437	GGTCGCTACTTCGATCTGCACTGGGAGTCGATGGTCAACATGCTTTCAC 256	

QY	241	TTCACACTGCATCTCGTGGCTCAAACAGACAGGTGTCATTGGACAACAGAG 300	Qy	241	TTCACACTGCATCTCGTGGCTCAAACAGACAGGTGTCATTGGACAACAGAG 300
Db	257	TTCCACTGCATCTCGTGGCTCAAACAGACAGGTGTCATTGGACAACAGAG 316	Db	241	TTCCACTGCATCTCGTGGCTCAAACAGACAGGTGTCATTGGACAACAGAG 300
QY	301	TGGGAATTCAAAAGTATGGCACTAG 327	Qy	301	TGGGAATTCAAAAGTATGGCACTAG 327
Db	317	TGGGAATTCAAAAGTATGGCACTAG 343	Db	301	TGGGAATTCAAAAGTATGGCACTAG 327
RESULT 22			RESULT 23		
B1858425	BT858425	549 bp mRNA linear EST 10-OCT-2001	B1858425	BU955646	550 bp mRNA linear EST 21-OCT-2002
LOCUS	603386437F1 NIH_MGC_87	mRNA clone IMAGE:5395281 5', mRNA sequence.	LOCUS	AGENCOURT 10612538 NIH_MGC_126	Homo sapiens cDNA clone
DEFINITION			DEFINITION	IMAGE:t72778 5'	mRNA Sequence.
ACCESSION	BI858425		ACCESSION	BU955646	
VERSION	BT858425..1	GI:159991912	VERSION	BU955646..1	GI:24185218
KEYWORDS			KEYWORDS		
SOURCE	Homo sapiens (human)		SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens		ORGANISM	Homo sapiens	
	Mammalia; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo				
REFERENCE	1 (bases 1 to 549)		REFERENCE	1 (bases 1 to 550)	
AUTHORS	NTH-MGC	http://mgc.nci.nih.gov/	AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)		JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabps@nih.nih.gov		COMMENT	Email: cgabps@nih.nih.gov Tissue Procurement: NCI CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LInL) DNA Sequencing by: Incyte Genomics, Inc.	
REFERENCE	1 (bases 1 to 549)		REFERENCE	1 (bases 1 to 550)	
AUTHORS	NTH-MGC	http://mgc.nci.nih.gov/	AUTHORS	NIH-MGC	http://mgc.nci.nih.gov/
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)		JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabps@nih.nih.gov		COMMENT	Email: cgabps@nih.nih.gov Tissue Procurement: NCI CDNA Library Preparation: Michael Brownstein Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LInL) DNA Sequencing by: Incyte Genomics, Inc.	
FEATURES	source		FEATURES	source	
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	/mol_type="mRNA"			/mol_type="mRNA"	
	/db_xref="taxon:9606"			/db_xref="taxon:9606"	
	/clone="IMAGE:5395281"			/clone="IMAGE:677878"	
	/tissue_type="mammary adenocarcinoma, cell line"			/tissue_type="mixed (pool of 40 RNAB)"	
	/lab_host="DH10B (phage-resistant)"			/lab_host="DH10B (T1-phage-resistant)"	
	/clone_lib="NIH_MGC_87"			/clone_lib="NIH_MGC_126"	
	/note="Organ: breast" Vector: PCMV-SPORT6; Site 1: NotI;			/note=Vector: pBNR-LIB; Site 1: Sf11 (ggccattatggcc);	
	Site 2: SalI; Cloned unidirectionally; oligo-dT primed.			Site 2: Sf11 (ggccgttcggcc); Double-stranded DNA was prepared from a pool of 40 cell line poly+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%)	
	Average insert size 1.383 kb. Library enriched for full-length clones and constructed by Life Technologies.			adaptors were used in cloning as follows: 5'-AAGCAGTGTATCACGAGTGGCCATTGCCGG-3', and 5'-ATTCAGAGGCCGGGAGATGGATTCATGGCTTGTG-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH_MGC_127 and NIH_MGC_128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC Library."	
	Note: this is a NIH_MGC Library."				
ORIGIN			Query Match	100 0%	Score 327; DB 5; Length 549;
	Best Local Similarity 100.0%	Pred. No. 6..6e-175;	Matches	0; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 100.0%; Pred. No. 6..6e-175;
	Matches 327; Conservative 0;			Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 ATGGCGCAGGGATGATGGATACTCCAGCGCACCACAGGGCGGGAAAGAG 60		QY	1 ATGGCGCAGGGATGATGGATACTCCAGCGCACCACAGGGCGGGAAAGAG 60	
Db	1 ATGGCGCAGGGATGATGGATACTCCAGCGCACCACAGGGCGGGAAAGAG 60		Db	1 ATGGCGCAGGGATGATGGATACTCCAGCGCACCACAGGGCGGGAAAGAG 60	
QY	61 CGCTTGAACTGAAAGTGAATCGATGCCCTGGGATATTGTTGAT 120		QY	1 ATGGCGCAGGGATGATGGATACTCCAGCGCACCACAGGGCGGGAAAGAG 60	
Db	61 CGCTTGAACTGAAAGTGAATCGATGCCCTGGGATATTGTTGAT 120		Db	17 ATGGCGCAGGGATGATGGATACTCCAGCGCACCACAGGGCGGGAAAGAG 76	

Qy	61	CGCTTGTAACTGAAAGTGGATGCGTAGACCCCTGGGATATTGGTTGAT	120	
Qy	77	CGCTTGTAAAGTGGATGCGTAGACCCCTGGGATATTGGTTGAT	136	
Db	121	AACCTGGCCACTGCGGAAACACATATTGGATCTTGATAGTCAGCTAACCG	180	
Db	137	AACCTGGCCACTGCGGAAACACATATTGGATCTTGATAGTCAGCTAACCG	196	
Qy	181	GGTTCGGCTACTCTCAGAAGAGTGGTCACTGGAGCTGTGATGGGAGCTTTCAC	240	
Db	197	GGTTCGGCTACTCTCAGAAGAGTGGTCACTGGAGCTGTGATGGGAGCTTTCAC	256	
Qy	241	TTCACACTGCACTCTCCTGGCTCAAACACAGAGTGGTCCATTGGACACAGAG	300	
Db	257	TTCACACTGCACTCTCCTGGCTCAAACACAGAGTGGTCCATTGGACACAGAG	316	
Qy	301	TGGGAATTCCAAAAGTATGGGACTAG	327	
Db	317	TGGGAATTCCAAAAGTATGGGACTAG	343	
				RESULTS
	24	CD249363	554 bp	mRNA
	LOCUS	CD249363	554 bp	EST 22-MAY-2003
	DEFINITION	AGENCOURT_14100407 NIH_MGC_172 Homo sapiens cDNA 5'	, mRNA sequence.	
	ACCESSION	CD249363_1	GI:31009829	
	VERSION	CD249363_1	EST	
	KEYWORDS	Homo sapiens (human)		
	SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
	ORGANISM	National Institutes of Health, Mammalian Gene Collection (MGC)		
	REFERENCE	NIH/MGC http://mgc.nci.nih.gov/		
	AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)		
	TITLE	Unpublished (1999)		
	JOURNAL	Contract: Daniela S. Gerhard, Ph.D.		
	COMMENT	Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10407 Bethesda, MD 20892 Email: cgabbs-r@mail.nih.gov Tissue Procurement: Dr. Jamie Thompson, University of WI DNA Library Preparation: Gina Zastrow-Hayes DNA Library Arrayed by: The I.M.A.G.E. Consortium (LJNL)		
		DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LJNL at: <a href="http://image.ljnl.gov">http://image.ljnl.gov</a>		
		Plate: LJCN2728 row: o column: 10		
		High quality sequence stop: 530.		
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				/mol_type="mRNA"
				/db_xref="taxon:9606"
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				/clone lib=NIH_MGC_126"
				/note="Vector: pDONR-LIB; Site:1: SfiI (ggccattttggcc); Site:2: SfiI (ggccgtttggcc); Double-stranded DNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:
				5'-AGGCCGTTGATCTAACGCCAGACTGGCCATGGCCATGGCTGGG-3' and 5'-ATTCTAGGCCGAGCGGCCGATG-G-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH_MGC_127
				Query Match 100.0% Score 327; DB 6; Length 554;
				Best Local Similarity 100.0%; Pred. No. 6.6e-175; Mismatches 327; Conservative 0; Indels 0; Gaps 0;
Qy	1	ATGCCGGAGCGATGGATGCTGGATCCGGAGGGCACCAACGGGGGGCAAGAG	60	
Dh	34	ATGCCGGAGCGATGGATGCTGGATCCGGAGGGCACCAACGGGGGGCAAGAG	93	

and NIH\_MGC\_128). Library Created in the laboratory of T. Usdin, M.D., Ph.D. (NIH, NIH). Note: this is a NIH\_MGC Library."

prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were used in cloning as follows:

5'-AAGCTTGTATCAACCCAGACTGGCCATATTAGGGGG-3', and  
 5'-ATTCTAGGCCGAGGGCAGATG-dt(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the >0.5 kb size fraction (other fractions present in NIH-MGC-141). Library created in the laboratory of M. Brownstein (NIH, NIH). Note: this is a NIH MGC Library."

Db	73	CGCTTGAACTGAAAGTGAATCAGTAGCCCTGGGCTGGATATTGTTGTAT	132
Qy	121	AACCTGCCCCATCTGGAGAACCACTTATGGATCTTGCATAGAAATGTCAGAACCG	180
Db	133	AACCTGCCCCATCTGGAGAACCACTTATGGATCTTGCATAGAAATGTCAGAACCG	192
Qy	181	GCGTCGCPACTTCAAGAAGTGPACTGTGGCATGGGACTCTGTAACCATGCTCAC	240
Db	193	GCGTCGCPACTTCAAGAAGTGPACTGTGGCATGGGACTCTGTAACCATGCTCAC	252
Qy	241	TTCCAACTGZATCTCGCTCAAAAACCGAACAGGTGTCCATTGGACAACAGAGAG	300
Db	253	TTCCAACTGZATCTCGCTCAAAAACCGAACAGGTGTCCATTGGACAACAGAGAG	312
Qy	301	TGGGAATTCCAAAAGTATGGCACTAG	327
Db	313	TGGGAATTCCAAAAGTATGGCACTAG	339

RESULT	26	BU601080	BU601080	555 bp	mRNA	linear	EST	20-SEP-2002
LOCUS		AGENCOURT 1005891	NIH_MGC_142	Homo sapiens	cDNA clone			
DEFINITION		IMAGE 6494946 5'	mRNA sequence.					
ACCESSION		BU601080						
VERSION		BU601080.1	GI:23252839					
KEYWORDS		EST.						
SOURCE		Homo sapiens	(human)					
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
		Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;						
Hominidae; Homo.								
REFERENCE		1 (bases 1 to 555)						
AUTHORS		NIH-MGC http://mgc.nci.nih.gov/						
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)						
JOURNAL		Unpublished (1999)						
COMMENT		Contact: Robert Strausberg, Ph.D.						
		Email: cgbbs@mail.nih.gov						
TISSUE		Tissue Procurement: Michael Brownstein Laboratory						
		CDNA Library Preparation: Michael Brownstein Laboratory						
		CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LJNL)						
DNA Sequencing by:		Agenocyte Bioscience Corporation						
Clone distribution:		MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LJNL at:						
		<a href="http://image.ljnl.org">http://image.ljnl.org</a>						
Plate:		LICM2671 row: p column: 19						
		High quality sequence stop: 510.						

FEATURES	source	Location/Qualifiers
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FEATURES source	COMMENT																																								
Location/Qualifiers <ul style="list-style-type: none"> <li>1. .557</li> <li>/organism="Homo sapiens"</li> <li>/mol_type="mRNA"</li> <li>/db_xref="Taxon:9606"</li> <li>/clone="IMAGE:6726227"</li> <li>/tissue_type="mixed (pool of 40 RNAs)"</li> <li>/lab_host="DH10B (T1-phage-resistant)"</li> <li>/clone_lab="NIH MGC_126"</li> <li>/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc); Site 2: SfiI (ggccgcctcgcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%, kidney - 2.2%, liver - 5.7%, lung - 10.4%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%) 5, and 3' adaptors were used in cloning as follows: 5'-AAGCACTGTTATCACGGAGTGCGCATTAACGCCGCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-1 kb size fraction (other fractions present in NIH MGC_127 and NIH MGC_128). Library created in the laboratory of T. Urdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC Library."</li> </ul>	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A/7 Bethesda, MD 20892 Email: ccapbs-r@mail.nih.gov Tissue Procurement: Dr. Gina Zastrow-Hayes CDNA Library Preparation: Gina Zastrow-Hayes DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov/plate: NDKM80 row: h column: 04 /db_xref="Taxon:9606"																																								
FEATURES source	<p>High quality sequence start: 13 High quality sequence stop: 558.</p> <p>Location/Qualifiers           <ul style="list-style-type: none"> <li>1. .558</li> <li>/organism="Homo sapiens"</li> <li>/mol_type="mRNA"</li> <li>/db_xref="Taxon:9606"</li> <li>/tissue_type="embryonic trophoblasts, made from WA01 stem cells"</li> <li>/lab_host="DH10B TonA"</li> <li>/clone_lib="NIH_MGC_173"</li> <li>/note="Vector: pDNR201; Site 1: attP2; Site 2: attP1; LIBR_PRIMING - Oligo dt; METHOD - Full-length enriched LIBR_PROVIDER - Bradfield"</li> </ul> </p>																																								
ORIGIN	<p>Query Match Score 327; DB 5; Length 557;</p> <table border="1"> <thead> <tr> <th>Query</th> <th>Match Score</th> <th>DB</th> <th>Length</th> </tr> </thead> <tbody> <tr> <td>Qy</td> <td>100.0%</td> <td>6</td> <td>558;</td> </tr> <tr> <td>Qy</td> <td>100.0%</td> <td>6.6e-175;</td> <td>Pred. No. 6.6e-175;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Mismatches</td> <td>0;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Indels</td> <td>0;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Gaps</td> <td>0;</td> </tr> <tr> <td>Qy</td> <td>100.0%</td> <td>0</td> <td>0;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Mismatches</td> <td>0;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Indels</td> <td>0;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Gaps</td> <td>0;</td> </tr> </tbody> </table> <p>Best Local Similarity 100.0% Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <ul style="list-style-type: none"> <li>1 ATGGGGCGCGGAGTGTGATAACCCGGCGCAACACGGGGGGAGAGAG 60</li> <li>22 ATGGGGCGAGCGGATGGATGTGGATAACCCGGCGCAACACGGGGGGCAAGAG 81</li> <li>61 CGCTTGTAACTGAAAATGTGAAATCGTAGGCCCTCTGGCTGGATAATTGGTTGAT 120</li> <li>82 CGCTTGTAACTGAAAATGTGAAATGGTGAATGGTGAATGGCTGGATTTGTGT 141</li> <li>121 AACCTGCCATCTGGAGAACCATTAATTGATCTTGGCATAGATGTCAGCTAACAG 180</li> <li>142 AACCTGCCATCTGGAGAACCATTAATTGATCTTGGCATAGATGTCAGCTAACAG 201</li> <li>181 GCGTGGCCTACTCGAGAGTCAAGGTGACTCTGCGATGGGAGTCCTAACATGCTTCAC 240</li> <li>202 GCGTGGCCTACTCGAGAGTGTACTCTGCGATGGGAGTCCTAACATGCTTCAC 261</li> <li>241 TTCCACTGCACTCTCGCTGTCTGCTAAAAACAGCAAGGTGTCTGATGACAACAGAG 300</li> <li>262 TTCCACTGCACTCTCGCTGTCTGCTAAAAACAGCAAGGTGTCTGATGACAACAGAG 321</li> <li>301 TGGGAATTCAAAAGTATGGCACTAG 327</li> <li>322 TGGGAATTCAAAAGTATGGCACTAG 348</li> </ul>	Query	Match Score	DB	Length	Qy	100.0%	6	558;	Qy	100.0%	6.6e-175;	Pred. No. 6.6e-175;	Db	0	Mismatches	0;	Db	0	Indels	0;	Db	0	Gaps	0;	Qy	100.0%	0	0;	Db	0	Mismatches	0;	Db	0	Indels	0;	Db	0	Gaps	0;
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Db	0	Mismatches	0;																																						
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Db	0	Gaps	0;																																						
RESULT 28 CD388268	<p>Query Match Score 327; DB 5; Length 557;</p> <table border="1"> <thead> <tr> <th>Query</th> <th>Match Score</th> <th>DB</th> <th>Length</th> </tr> </thead> <tbody> <tr> <td>Qy</td> <td>100.0%</td> <td>6</td> <td>557;</td> </tr> <tr> <td>Qy</td> <td>100.0%</td> <td>6.6e-175;</td> <td>Pred. No. 6.6e-175;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Mismatches</td> <td>0;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Indels</td> <td>0;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Gaps</td> <td>0;</td> </tr> <tr> <td>Qy</td> <td>100.0%</td> <td>0</td> <td>0;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Mismatches</td> <td>0;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Indels</td> <td>0;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Gaps</td> <td>0;</td> </tr> </tbody> </table> <p>Best Local Similarity 100.0% Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <ul style="list-style-type: none"> <li>1 (bases 1 to 558)</li> </ul>	Query	Match Score	DB	Length	Qy	100.0%	6	557;	Qy	100.0%	6.6e-175;	Pred. No. 6.6e-175;	Db	0	Mismatches	0;	Db	0	Indels	0;	Db	0	Gaps	0;	Qy	100.0%	0	0;	Db	0	Mismatches	0;	Db	0	Indels	0;	Db	0	Gaps	0;
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Db	0	Mismatches	0;																																						
Db	0	Indels	0;																																						
Db	0	Gaps	0;																																						
RESULT 29 CK003869	<p>Query Match Score 327; DB 5; Length 559;</p> <table border="1"> <thead> <tr> <th>Query</th> <th>Match Score</th> <th>DB</th> <th>Length</th> </tr> </thead> <tbody> <tr> <td>Qy</td> <td>100.0%</td> <td>6</td> <td>559;</td> </tr> <tr> <td>Qy</td> <td>100.0%</td> <td>6.6e-175;</td> <td>Pred. No. 6.6e-175;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Mismatches</td> <td>0;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Indels</td> <td>0;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Gaps</td> <td>0;</td> </tr> <tr> <td>Qy</td> <td>100.0%</td> <td>0</td> <td>0;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Mismatches</td> <td>0;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Indels</td> <td>0;</td> </tr> <tr> <td>Db</td> <td>0</td> <td>Gaps</td> <td>0;</td> </tr> </tbody> </table> <p>Best Local Similarity 100.0% Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p> <ul style="list-style-type: none"> <li>1 (bases 1 to 559)</li> </ul>	Query	Match Score	DB	Length	Qy	100.0%	6	559;	Qy	100.0%	6.6e-175;	Pred. No. 6.6e-175;	Db	0	Mismatches	0;	Db	0	Indels	0;	Db	0	Gaps	0;	Qy	100.0%	0	0;	Db	0	Mismatches	0;	Db	0	Indels	0;	Db	0	Gaps	0;
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Db	0	Mismatches	0;																																						
Db	0	Indels	0;																																						
Db	0	Gaps	0;																																						
DEFINITION AGENCOURT_14304357 NIH_MGC_173 Homo sapiens cDNA 5 , mRNA sequence.	DEFINITION AGENCOURT_16389678 NIH_MGC_228 Homo sapiens cDNA clone IMAGE_3071640 5' , mRNA sequence.																																								
ACCESSION CD388268	ACCESSION CK003869																																								
KEYWORDS EST.	KEYWORDS CK003869.1 GI:38529903																																								
SOURCE Homo sapiens (human)	SOURCE Homo sapiens (human)																																								
ORGANISM Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo	ORGANISM Eukarya; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea; Homo																																								
REFERENCE NIH-MGC http://mgc.ncbi.nih.gov/	REFERENCE NIH-MGC Unpublished (1999)																																								
AUTHORS	AUTHORS																																								
TITLE	TITLE																																								
JOURNAL	JOURNAL																																								

TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	KEYWORDS	EST, Homo sapiens (human)
JOURNAL	Unpublished (1999)	SOURCE ORGANISM	Homo sapiens
COMMENT	Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NIH Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: ccapbs-r@mail.nih.gov Tissue Procurement: Professor Mikliss Palkovits cDNA Library Preparation: Michael Brownstein / Ted Usdin Laboratory Arrived by: The I.M.A.G.E. Consortium (LNL) cDNA Library Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>	REFERENCE	NIH-MGC http://mgc.nci.nih.gov/.
FEATURES		AUTHORS	1 (bases 1 to 562)
source		JOURNAL	Unpublished (1999)
FEATURES		COMMENT	Contact: Robert Straussberg, Ph.D. Email: cgaps-r@mail.nih.gov Tissue Procurement: Dr. Jamie Thompson, University of WI cDNA Library Preparation: Gina Zastrow-Hayes cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>
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FEATURES			/clone="IMAGE:1071940"
source			/tissue_type="Human Brain - Cerebellar Cortex"
FEATURES			/lab_host="DH10B TONA"
source			/clone_id="NIH_MGC_228"
FEATURES			/note="Organ: brain/CNS; Vector: PDNR-LIB; Site 1: SfII (directional); Site 2: SfII (directional); Library is oligo-dT primed and directionally cloned.; 5' and 3' adaptors were used in cloning as follows: 5'-AGGCAGGGATCAACCCAGACTGGCCATAGCGCGGG-3'5'-ATCTCTAGAGGG CCGAGGGCGGCCGACGT-dT) 3N 1N-3. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected for >0.5kb with an average insert size of 1.2kb Library created in the laboratory of Jonathan Kuo and Ted Usdin."
ORIGIN		ORIGIN	
	Query Match 100.0%; Score 327; DB 7; Length 559;	Query Match 100.0%; Score 327; DB 6; Length 562;	
	Best Local Similarity 100.0%; Pred. No. 6.6e-175; Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Best Local Similarity 100.0%; Pred. No. 6.6e-175; Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 ATGGCCGAGGGATGGATGGATACTCCAGCCAGCGGCCAACAGCCGCGGCCAGAAAG 60	Qy 1 ATGGCCGAGGGATGGATGGATACTCCAGCCAGCGGCCAACAGCCGCGGCCAGAAAG 60	
Db	23 ATGGCCGAGGGATGGATGGATACTCCAGCCAGCGGCCAACAGCCGCGGCCAGAAAG 82	Db 40 ATGGCCGAGGGATGGATGGATACTCCAGCCAGCGGCCAACAGCCGCGGCCAGAAAG 99	
Qy	61 CGCTTTCGAAGTCAAAGTGGAAATGGCTCTGGCCTGGGATATGGTTGAT 120	Qy 61 CGCTTTCGAAGTCAAAGTGGAAATGGCTCTGGCCTGGGATATGGTTGAT 120	
Db	83 CGCTTTCGAAGTCAAAGTGGAAATGGCTCTGGCCTGGGATATGGTTGAT 142	Db 100 CGCTTTCGAAGTCAAAGTGGAAATGGCTCTGGCCTGGGATATGGTTGAT 159	
Qy	121 AACTGTGCCCATCTGAGGAACCACATATGGATCTTGCATAGAAATGGCTAACAGC 180	Qy 121 AACTGTGCCCATCTGAGGAACCACATATGGATCTTGCATAGAAATGGCTAACAGC 180	
Db	143 AACTGTGCCCATCTGAGGAACCACATATGGATCTTGCATAGAAATGGCTAACAGC 202	Db 181 GCGTCCGCTACTTCAGAAGACTGTACTGCGATGGGAGCTGTGCTGTTTCAC 240	
Qy	181 GCGTCCGCTACTTCAGAAGACTGTACTGCGATGGGAGCTGTGCTGTTTCAC 240	Db 220 GCGTCCGCTACTTCAGAAGACTGTACTGCGATGGGAGCTGTGCTGTTTCAC 279	
Db	203 GGTCCCTACTTCAGAAGACTGTACTGCGATGGGAGCTGTGCTGTTTCAC 262	Qy 241 TTCACTGCATCTCTGGCTGGCTCAAACAGCACGGTGCTCATGGACACAGAG 300	
Qy	241 TTCCACTGCATCTCTGGCTGGCTCAAACAGCACGGTGCTCATGGACACAGAG 300	Db 280 TTCACTGCATCTCTGGCTGGCTCAAACAGCACGGTGCTCATGGACACAGAG 339	
Db	263 TTCCACTGCATCTCTGGCTGGCTCAAACAGCACGGTGCTCATGGACACAGAG 322	Qy 301 TGGGAATTCCAAAAGTGGGACTAG 327	
Qy	301 TGGGAATTCCAAAAGTGGGACTAG 327	Db 340 TGGGAATTCCAAAAGTGGGACTAG 366	
Db	323 TGGGAATTCCAAAAGTGGGACTAG 349	RESULT 31	
		BUB61191	
		LOCUS	563 bp mRNA linear EST 16-OCT-2002
		DEFINITION	AGENCOURT_13976103 NIH_MGC_172 Homo sapiens cDNA clone
		ACCESSION	IMAGE:652636 5', mRNA sequence.
		VERSION	BUB61191
		KEYWORDS	GI:24046183
		SOURCE	EST.
			Homo sapiens (human)



Qy	181	GCGTCCGCTACTCAGAACAGTGTACTTCGCATGGGAGTCAGTGTACCATGCTTTAC	240	Qy	1	ATGGCGGAAGCGATTGGATAACCCGAGGGCACCAACAGCGGCCGCGGCCAAGAG	60				
Db	212	GCGTCCGCTACTCAGAACAGTGTACTTCGCATGGGAGTCAGTGTACCATGCTTTAC	271	Db	38	ATGGCGGCAGCGATTGGATAACCCGAGGGCACCAACAGCGGCCGCGGCCAAGAG	97				
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Db	272	TTCACATGATCTCTGGCTCAAAACAGACAGGGTGTCATGACAACAGGGAG	331	Db	98	CGGTTGAAGTAAAAGTGGATGAGTAGCCTCTGGCTGGGATATTGGTTGAT	157				
Qy	301	TGGGAATTCCAAGATGGGCACTAG	327	Qy	121	AACGTGTCATCTGCAGAACCAATTGGATGAGTAGCAAGTAACCAACAG	180				
Db	332	TGGGAATTCCAAGATGGGCACTAG	358	Db	158	AACGTGTCATCTGCAGAACCAATTGGATGAGTAGCAAGTAACCAACAG	217				
<b>RESULT 33</b>											
BU533405	BU533405	573 bp mRNA linear EST 13-SEP-2002		Qy	181	GCCTCCGCTACTCTAGAGAGTGTACTTCGATGGGAGTCGATGCTTCAC	240				
LOCUS	AGENCOURT_10197885	NIH_MGC_126 Homo sapiens cDNA clone		Db	218	GCCTCCGCTACTCTAGAGAGTGTACTTCGATGGGAGTCGATGCTTCAC	277				
DEFINITION	IMAGE:655746 5'	mRNA sequence.		Qy	241	TTCACATGATCTCTGGCTCAAACACAGTCATGGACACAGAG	300				
ACCESSION	BU533405			Db	278	TTCACATGATCTCTGGCTCAAACACAGTCATGGACACAGAG	337				
VERSION	BU533405.1	GI:22843846		Qy	301	TGGGAATTCCAAGATGGGCACTAG	327				
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ORGANISM	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.			<b>RESULT 34</b>							
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AUTHORS	NIH_MGC http://mgc.nci.nih.gov/			LOCUS	BP308845	Sugano cDNA library, brain Homo sapiens cdNA clone					
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			DEFINITION	BP308845	mRNA sequence.					
JOURNAL	Unpublished (1999)			ACCESSION	NRB06593	mRNA sequence.					
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgdpbs@mail.nih.gov			VERSION	BP308845.1	GI:52237818					
Tissue Procurement:	NCI			KEYWORDS	EST.						
CDNA Library Preparation:	Michael Brownstein Laboratory			SOURCE	Homo sapiens (human)						
CDNA Library Arrayed by:	The I.M.A.G.E. Consortium (ILNL)			ORGANISM	Bukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.						
DNA Sequencing by:	Agencourt Bioscience Corporation			REFERENCE	1 (bases 1 to 581)						
Clone distribution:	MGC clone distribution information can be found through the J.M.A.G.E. Consortium/ILNL at:			AUTHORS	Suzuki,Y., Yanashita,R., Shirota,M., Sakakibara,Y., Chiba,J., Mizushima-Sugano,J., Nakai,K. and Sugano,S.						
Plate:	LICM2731 row: h column: 18			TITLE	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions						
High quality sequence stop:	544.			JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)						
Location/Qualifiers	1..573			PUBMED	15342556						
/organism="Homo sapiens"				COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan Email: yszuki@ims.u-tokyo.ac.jp.						
/mol type="mRNA"				FEATURES	581	Location/Qualifiers					
/db_xref="taxon:9606"				Source	/organism="Homo sapiens"						
/clone="IMAGE:6559746"					/mol type="mRNA"						
/tissue type="mixed (pool of 40 RNAs)"					/db_xref="taxon:9606"						
/lab_host="DH10B (T1-phage-resistant)"					/clone="NRB06593"						
/clone lib="NIH_MGC_126"					/tissue type="brain"						
<b>ORIGIN</b>											
Query Match	100.0%	Score 327; DB 3; Length 581;									
Best Local Similarity	100.0%	Pred. No. 6-6e-175;									
Matches	327;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1	ATGGCGGCAGCGATGGATGTTGGATAACCCGAGGGACACAAACGCCGCCAGCAAGAG	60								
Db	14	ATGGCGGCAGCGATGGATGTTGGATAACCCGAGGGACACAAACGCCGCCAGCAAGAG	73								
<b>ORIGIN</b>											
Query Match	100.0%	Score 327; DB 5; Length 573;									
Best Local Similarity	100.0%	Pred. No. 6.6e-175;									
Matches	327;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;									

Qy	121	AACTGTGCCATCTGAGAACCAACATATTGATCCTTGCATAAGTCAGTAACTCG 180	Db	252	TTCACGTGATCTCTGGCTCAAAACGACAGGAGTCATTTGACAGAGAG 311	
Db	134	AACTGTGCCATCTGAGAACCAACATATTGATCCTTGCATAAGTCAGTAACTCG 193	Qy	301	TGGGAATTCCAAAATGTCATGGGACTAGCTGTAACCATGCTTTCAC 327	
Qy	181	GCTTCGGCTACTTCAGAGAGTGACTCTGCAATGGGAGTCGTAACTGCTTTCAC 240	Db	312	TGGGAATTCCAAAATGTCATGGGACTAGCTGTAACCATGCTTTCAC 338	
Db	194	GCTTCGGCTACTTCAGAGAGTGACTCTGCAATGGGAGTCGTAACTGCTTTCAC 253				
Qy	241	TTCACATGCCATCTCTCGTGGCTCAAACAGCACAGCTGTCATGGCAACAGAGAG 300			RESULT 36	
Db	254	TTCACATGCCATCTCTCGTGGCTCAAACAGCACAGCTGTCATGGCAACAGAGAG 313	Qy	301	TGGGAATTCCAAAAGTAGTGGCACTAG 327	
Qy	314	TGGGAATTCCAAAAGTAGTGGCACTAG 340	Db	312	TGGGAATTCCAAAAGTAGTGGCACTAG 340	
Qy	BP317451	BP317451 Sugano cDNA library, EST 17-SEP-2004	Db	BP317451 Sugano cDNA library, EST 17-SEP-2004	LOCUS	
DEFINITION	PCD03725, mRNA sequence.	LOCUS	BP317451 Sugano cDNA library, EST 17-SEP-2004	DEFINITION		
ACCESSION	BP317451	ACCESSION	BP317451 Sugano cDNA library, EST 17-SEP-2004	ACCESSION		
VERSION	GI:52246426	VERSION	GI:52246426	VERSION		
SOURCE	Homo sapiens (human)	SOURCE	Homo sapiens (human)	SOURCE		
ORGANISM	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	ORGANISM	Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	ORGANISM		
REFERENCE	1 (bases 1 to 583)	REFERENCE	1 (bases 1 to 583)	REFERENCE		
AUTHORS	Suzuki,Y.,Yamashita,R.,Shirota,M.,Sakakibara,Y.,Chiba,J., Mizushima-Sugano,J.,Nakai,K. and Sugano,S.	AUTHORS	Suzuki,Y.,Yamashita,R.,Shirota,M.,Sakakibara,Y.,Chiba,J., Mizushima-Sugano,J.,Nakai,K. and Sugano,S.	AUTHORS		
TITLE	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions	TITLE	Sequence comparison of human and mouse genes reveals a homologous block structure in the promoter regions	TITLE		
JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)	JOURNAL	Genome Res. 14 (9), 1711-1718 (2004)	JOURNAL		
PUBMED	15343556	PUBMED	15343556	PUBMED		
COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan Email: yutaki@ims.u-tokyo.ac.jp. Location/Qualifiers	COMMENT	Contact: Yutaka Suzuki Department of Virology Institute of Medical Science, University of Tokyo 4-6-1, Shirokanedai, Minato-ku, Tokyo 108-8639, Japan Email: yutaki@ims.u-tokyo.ac.jp. Location/Qualifiers	COMMENT		
FEATURES	1 .583	FEATURES	1 .583	FEATURES		
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	/lab_host="IDH10"		/lab_host="IDH10"			
	/clone lib="NIH MGC_96"		/clone lib="NIH MGC_96"			
	/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: Sall-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTN-3', size selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."		/note="Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site 1: BamHI; Site 2: Sall-XhoI (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTN-3', size selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."			
ORIGIN		ORIGIN		ORIGIN		
Query Match	100.0%	Query Match	100.0%	Query Match		
Best Local Similarity	100.0%	Best Local Similarity	100.0%	Best Local Similarity		
Matches 327;	Conservative 0;	Matches 327;	Conservative 0;	Matches 327;		
	Mismatches 0;		Mismatches 0;			
	Indels 0;		Indels 0;			
	Gaps 0;		Gaps 0;			
Qy	1	ATGCCGGCGCGGATGGATGGAPACCCCGAGGGCACC2ACAGCGCCGGCAAGAAG 60	Qy	1	ATGCCGGCGCGGATGGATGGAPACCCCGAGGGCACC2ACAGCGCCGGCAAGAAG 71	ORIGIN
Db	12	ATGCCGGCGCGGATGGATGGAPACCCCGAGGGCACC2ACAGCGCCGGCAAGAAG 71	Db	12	ATGCCGGCGCGGATGGATGGAPACCCCGAGGGCACC2ACAGCGCCGGCAAGAAG 71	ORIGIN
Qy	61	CGCTTTGAGTGAAAGTGGAATCGAGGCCCTCTGGGATATTGTGGTTGAT 120	Qy	1	ATGGCGCGAGGATGGATGGCTGGGACGCCACAGCGCCGGCAAGAAG 60	Query Match
Db	72	CGCTTTGAGTGAAAGTGGAATCGAGGCCCTCTGGGATATTGTGGTTGAT 131	Db	19	ATGGCGCGAGGATGGATGGCTGGGACGCCACAGCGCCGGCAAGAAG 78	Query Match
Qy	121	AACCTGTGCCATCTGAGAACCACTTATGGATCTTGCATAGATGTCAAGCTAACAG 180	Qy	1	CGCTTTGAGTGAAAGTGGAATCGAGGCCCTCTGGGATATTGTGGTTGAT 120	Best Local Similarity
Db	132	AACCTGTGCCATCTGAGAACCACTTATGGATCTTGCATAGATGTCAAGCTAACAG 191	Db	79	CGCTTTGAGTGAAAGTGGAATGGCTGGGACGCCACAGCGCCGGCAAGAAG 138	Best Local Similarity
Qy	181	GCGTCGGCTACTTCAGAGAGTGACTCTGGGACTCTGTAACCATGCTTTCAC 240	Qy	121	AACCTGTGCCATCTGAGAACCACTTATGGATCTTGCATAGATGTCAAGCTAACAG 180	Matches 327;
Db	192	GCGTCGGCTACTTCAGAGAGTGACTCTGGGACTCTGTAACCATGCTTTCAC 251	Db	139	AACTGTGCCATCTGAGAACCACTTATGGATCTTGCATAGATGTCAAGCTAACAG 198	Matches 327;
Qy	241	TTTCACTGAGACTCTCGGCTCAAACACGAGCAGGGTGTCCATTGGACACAGAGAG 300	Qy			Length 616;



Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 100.0%; Score 327; DB 5; Length 801;

Best Local Similarity 100.0%; Pred. No. 6.8e-175;

Mismatches 0; Indels 0; Gaps 0;

Matches 327; Conservative 0; Gaps 0;

1 ATGGGGCACGGATGATGGATACTGGATGTCAGCTGGAAAGAG 60

44 ATGGGGCACGGATGATGGATACTGGATCAGCGGGCAAGAG 103

61 CGCTTGTAGTGAAAGGTGAATGCTAGCCCTCTGCCCTGGATAATTGTGTGAT 120

Db 104 CGCTTGTAGTGAAAGGTGAATGCTAGCCCTCTGCCCTGGATAATTGTGTGAT 163

Qy 121 AACGTGCTCATCTGAGGACCACTATTGATGTTGATAGATGTAAGGTAACAG 180

Db 164 AACGTGCTCATCTGAGGACCACTATTGATGTTGATAGATGTAACAG 223

Qy 181 CGGTGGCTACTTCGAAAGGTGTACTGTCGATGGACTCTGAACTATGTTAAC 240

Db 224 GGTGCGCTACTTCGAAAGGTGTACTGTCGATGGACTCTGAACTATGTTAAC 283

Qy 241 TTCCACTGCACTCTCGCTGGCTCAAACACGACAGGTGTCCATTGACAACAGAG 300

Db 284 TTCCACTGCACTCTCGCTGGCTCAAACACGACAGGTGTCCATTGACAACAGAG 343

Qy 301 TGGGAATTCCTAAAGTAGGGCACTAG 327

Db 344 TGGGAATTCCTAAAGTAGGGCACTAG 370

RESULT 39

BUS959349 AGNCOURT\_10622637 NIH\_MGC\_127 Homo sapiens cDNA clone IMAGE:6737564 5', mRNA sequence.

DEFINITION BUS959349.1 GI:2418921

EST.

Homo sapiens (human)

ORGANISM Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominoidea; Homo.

1 (bases 1 to 845)

REFERENCE NIH-MGC http://mgc.ncbi.nih.gov/

AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE Unpublished (1999)

JOURNAL Contact: Robert Strausberg, Ph.D.

Email: cgbps-r@mail.nih.gov

Tissue Procurement: NCI

cDNA Library Preparation: Michael Brownstein Laboratory

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

<http://image.llnl.gov>

Plate: LICM3067 row: m column: 19

High quality sequence stop: 424.

Location/Qualifiers

1. 845 /organism="Homo sapiens"

/mol\_type="mRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:6737564"

/tissue="mixed (pool of 40 RNAs)"

/lab\_host="DH10B (T1-phage-resistant)"

/clone\_id="NIH MGC 127"

/note="Vector: PDR-NIB; Site 1: SfII (ggccattatggcc);

Site 2: SfII (ggccggctcgccc); Double-stranded cDNA was

prepared from a pool of 40 cell line polyA+ RNAs (bladder

- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon - 4%, connective tissue - 1.4%, eye - 1%, lung - 10.8%, NK-cell - 5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary gland - 1.3%, and skin - 2.3%. 5, and 3, adaptors were used in cloning as follows:  
 5'-AAGGAGCTATCAACGAGAGNGCCATACGCCGG-3', and 5'-ARTCTAGGCCCCGGCCGCGATG-DT(30>NN-3'). Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 1-2 kb size fraction (other fractions present in NIH MGC 126 and NIH MGC 128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH\_MGC Library."

## ORIGIN

Query Match 100.0%; Score 327; DB 5; Length 845;

Best Local Similarity 100.0%; Pred. No. 6.8e-175;

Mismatches 0; Indels 0; Gaps 0;

Matches 327; Conservative 0; Gaps 0;

1 ATGGGGCACGGATGATGGATACTGGATGTCAGCTGGAAAGAG 60

44 ATGGGGCACGGATGATGGATACTGGATCAGCGGGCAAGAG 103

61 CGCTTGTAGTGAAAGGTGAATGCTAGCCCTCTGCCCTGGATAATTGTGTGAT 120

Db 104 CGCTTGTAGTGAAAGGTGAATGCTAGCCCTCTGCCCTGGATAATTGTGTGAT 163

Qy 121 AACGTGCTCATCTGAGGACCACTATTGATGTTGATAGATGTAAGGTAACAG 180

Db 164 AACGTGCTCATCTGAGGACCACTATTGATGTTGATAGATGTAACAG 223

Qy 181 CGGTGGCTACTTCGAAAGGTGTACTGTCGATGGACTCTGAACTATGTTAAC 240

Db 224 GGTGCGCTACTTCGAAAGGTGTACTGTCGATGGACTCTGAACTATGTTAAC 283

Qy 241 TTCCACTGCACTCTCGCTGGCTCAAACACGACAGGTGTCCATTGACAACAGAG 300

Db 284 TTCCACTGCACTCTCGCTGGCTCAAACACGACAGGTGTCCATTGACAACAGAG 343

Qy 301 TGGGAATTCCTAAAGTAGGGCACTAG 327

Db 344 TGGGAATTCCTAAAGTAGGGCACTAG 370

RESULT 40

BG481544 LOCUS BG481544

DEFINITION 60252856F1 NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:4632028 5', mRNA sequence.

ACCESSION BG481544

VERSION EST.

KEYWORDS Homo sapiens (human)

SOURCE Homo sapiens

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi;

Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominoidea; Homo.

1 (bases 1 to 886)

REFERENCE 1 (bases 1 to 886)

AUTHORS NIH-MGC http://mgc.ncbi.nih.gov/

TITLE NIH\_MGC\_21 Homo sapiens cDNA clone IMAGE:4632028 5', mRNA sequence.

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgbps-r@mail.nih.gov

Tissue Procurement: Ling Hong/Rubin Laboratory

cDNA Library Preparation: The I.M.A.G.E. Consortium (LINL)

cDNA Library Arrayed by: Incyte Genomics, Inc.

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

<http://image.llnl.gov>

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High quality sequence stop: 529.

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/mol\_type="mRNA"

/db\_xref="taxon:9606"

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/clone\_id="NIH MGC 127"

/note="Vector: PDR-NIB; Site 1: SfII (ggccattatggcc);

Site 2: SfII (ggccggctcgccc); Double-stranded cDNA was

prepared from a pool of 40 cell line polyA+ RNAs (bladder



FEATURES	source	FEATURES	source	Location/Qualifiers
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/organism="Homo sapiens"	Location/Qualifiers	/mol type="mRNA"		/mol type="mRNA"
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/db_xref="IMAGE:6049202"		/clone="IMAGE:6049202"		/clone="IMAGE:6049202"
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/lab_host="DH10B (phage-resistant)"		/clone_lib="NIH MGC_71"		/clone_lib="NIH MGC_71"
/clone_lib="NIH MGC_72"		/note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dR."		/note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dR."
/note="Organ: skin; Vector: PCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dR."		Average insert size 2.1 kb."		Average insert size 2.1 kb."
Average insert size 2 kb.	Library constructed by Life Technologies."	ORIGIN		
Query Match Score 327; DB 3; Length 945;		Query Match Score 327; DB 3; Length 1098;		
Best Local Similarity 100.0%; Pred. No. 6.9e-175;		Best Local Similarity 100.0%; Pred. No. 6.9e-175;		
Matches 327; Conservative 0; Nismatches 0; Indels 0; Gaps 0;		Matches 327; Conservative 0; Nismatches 0; Indels 0; Gaps 0;		
Qy 1 ATGGCGCAGGATGATACTGGATACCCAGGGCAACACAGGGCGGGAGAAG 60		Qy 1 ATGGCGCAGGATGATACTGGATACCCAGGGCAACACAGGGCGGGAGAAG 60		
Db 33 ATGGCGCAGGATGATACTGGATACCCAGGGCAACACAGGGCGGGAGAAG 92		Db 33 ATGGCGCAGGATGATACTGGATACCCAGGGCAACACAGGGCGGGAGAAG 92		
Qy 61 CGCTTGTAACTGAAAGGTGGAATGCAAGTACGCCCTGGGATATTGGCTGGAT 120		Qy 61 CGCTTGTAACTGAAAGGTGGAATGCAAGTACGCCCTGGGATATTGGCTGGAT 120		
Db 93 CGCTTGTAACTGAAAGGTGGAATGCAAGTACGCCCTGGGATATTGGCTGGAT 152		Db 93 CGCTTGTAACTGAAAGGTGGAATGCAAGTACGCCCTGGGATATTGGCTGGAT 152		
Qy 121 AACGTGCCCCATCTGGAGAACACATTATGATCTTCGATAGATGTAAGCTAACAG 180		Qy 121 AACGTGCCCCATCTGGAGAACACATTATGATCTTCGATAGATGTAAGCTAACAG 180		
Db 153 AACGTGCCCCATCTGGAGAACACATTATGATCTTCGATAGATGTAAGCTAACAG 212		Db 153 AACGTGCCCCATCTGGAGAACACATTATGATCTTCGATAGATGTAAGCTAACAG 212		
Qy 181 GCGTCCGTACTTCGAGACTGTACTGTCCTGGAGCTGTAACTATGTTTAC 240		Qy 181 GCGTCCGTACTTCGAGACTGTACTGTCCTGGAGCTGTAACTATGTTTAC 240		
Db 213 GCGTCCGTACTTCGAGACTGTACTGTCCTGGAGCTGTAACTATGTTTAC 272		Db 213 GCGTCCGTACTTCGAGACTGTACTGTCCTGGAGCTGTAACTATGTTTAC 272		
Qy 241 TTCCACTGCACTCTCGCTGGCTCAAAAACAGCACAGGTGTGTCATTGGACAACAGAG 300		Qy 241 TTCCACTGCACTCTCGCTGGCTCAAAAACAGCACAGGTGTGTCATTGGACAACAGAG 300		
Db 273 TTCCACTGCACTCTCGCTGGCTCAAAAACAGCACAGGTGTGTCATTGGACAACAGAG 332		Db 273 TTCCACTGCACTCTCGCTGGCTCAAAAACAGCACAGGTGTGTCATTGGACAACAGAG 332		
Qy 301 TGGGAATTCCAAGATGGCACTAG 327		Qy 301 TGGGAATTCCAAGATGGCACTAG 327		
Db 333 TGGGAATTCCAAGATGGCACTAG 359		Db 333 TGGGAATTCCAAGATGGCACTAG 359		
RESULT 43		Search completed: March 15, 2006, 11:25:40		
BQ050461	BQ050461	BQ050461	BQ050461	Job time : 3739 secs
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DEFINITION	5' mRNA sequence.			cDNA clone IMAGE:5784423
ACCESSION	BQ050461			
VERSION	BQ050461.1			
KEYWORDS				
SOURCE	Homo sapiens (human)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Hominoidea; Homo.			
COMMENT	Contact: Robert Straubberg, Ph.D. Email: cgsapbs-r@mail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: Llam12869 row: o column: 16 High quality sequence stop: 548.			
REFERENCE	1 (bases 1 to 1098)			
AUTHORS				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)			
JOURNAL	Unpublished (1999)			

GenCore version 5.1.7  
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 12:22:08 ; Search time 368.547 Seconds  
 (without alignments)  
 5913.368 Million cell updates/sec

Title: US-09-541-462B-1  
 Perfect score: 327  
 Sequence: 1 atgcggcagcgatggatgt.....tccaaaatgtggcactag 327

Scoring table: OLIGO\_NUC  
 Gapop\_60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 12

Total number of hits satisfying chosen parameters: 116703

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N\_Geneseq\_21:  
 1: geneseqn1980s:  
 2: geneseqn1990s:  
 3: geneseqn2000s:  
 4: geneseqn2001as:  
 5: geneseqn2001bs:  
 6: geneseqn2002as:  
 7: geneseqn2002bs:  
 8: geneseqn2003as:  
 9: geneseqn2003bs:  
 10: geneseqn2003ss:  
 11: geneseqn2003ab:  
 12: geneseqn2004ab:  
 13: geneseqn2004bs:  
 14: geneseqn2005s:  
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
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2	327	100.0	482	3	AAC0396	Aac0396 Human sec
3	327	100.0	506	12	ADQ87156	Adq87156 Human tum
4	327	100.0	506	12	ADQ87156	Adq87156 Human tum
5	327	100.0	506	12	ADQ84881	Adq84881 Human tum
6	327	100.0	508	3	AAA74978	Aaa74978 DNA encod
7	327	100.0	508	13	ACN40951	Acn40951 Tumour-as
8	325	99.4	476	9	ACH29979	Ach29979 Human tes
c 9	321	98.2	3726	13	ADSN9913	Adn9913 Human the
c 10	321	98.2	4543	11	ACN90161	Acn90161 Breast ca
c 11	320	97.9	503	12	ADQ9179	Adq9179 Human pro
c 12	308	94.2	4476	5	ABV25615	Abv25615 Human pro
c 13	296	90.5	311	14	ACI57420	aci57420 Human col
c 14	296	90.5	3484	12	ADF42103	Adf42103 Human Tes
c 15	296	90.5	3484	12	ADQ8564	Adq8564 Human sof
c 16	296	90.5	3484	13	ADQ80865	Adq80865 Human SPA
c 17	296	90.5	511	10	ADB7558	Adb7558 Prostate
c 18	296	90.5	5371	12	ADD23032	Add23032 Human sof
c 19	267	81.7	5347	6	AAS94844	Aas94844 Human DNA

## ALIGNMENTS

RESULT 1	
ID	AAA6882 standard; DNA; 327 BP.
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AC	AAA96882;
XX	
DT	19-FEB-2001 (first entry)
XX	
DE	Nucleotide sequence of human ring finger protein ROC1.
XX	
KW	ROC1; Roc2; cullin; ring finger protein; APC complex; SCF pathway;
KW	cullin dependent ubiquitin ligase; CDK inhibitor Sic1 degradation; tumour; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key CDS
FT	1..327
FT	/tag= a /product= "ROC1"
XX	
XX	Location/Qualifiers
XX	1..327
XX	
XX	W020058472-A2.
XX	
PD	05-OCT-2000.
PF	31-MAR-2000; 20000W0-US008592.
XX	
PR	31-MAR-1999; 99US-0127261P.
PR	22-NOV-1999; 99US-0166927P.
XX	
PA	(UNNC-) UNIV NORTH CAROLINA.
XX	
PI	Xiong Y, Ohta T;
XX	
DR	WPI; 2000-647235/62.
DR	P-PSDB; AAB19160.
XX	
PT	Novel nucleic acid encoding cullin regulating ring finger proteins, termed as ROC proteins similar to anaphase-promoting complex 11, for therapeutic and diagnostic use.
XX	
PS	Claim 1; Fig 2A; 83pp; English.

XX The present sequence encodes a human ROC1 ring finger protein. The  
 CC specification also describes human ROC2. ROC1 and ROC2 are similar to  
 CC APC11, a subunit of the APC complex. The proteins stimulate cullin  
 CC dependent ubiquitin ligase activity. ROC1 functions in vivo as an  
 CC essential regulator of CDK inhibitor Sic1 degradation by the SCF  
 CC (undefined) pathway. ROC proteins are useful for screening bioactive  
 CC agents that interfere with the binding of ROC proteins with cullin  
 CC proteins. Pharmaceutical formulations comprising ROC proteins are useful  
 CC for diagnostic and therapeutic purposes, preferably for diagnosing and  
 CC treating tumours

XX Sequence 327 BP; 85 A; 75 C; 94 G; 73 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 327; DB 3; Length 327;  
 XX Best Local Similarity 100.0%; Pred. No. 2.6e-157;

XX Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCCAGCGATGGATGTGGATACCCGAGGGCACCAACCGGGCCAAAGAG 60  
 Db 1 ATGGCGCCAGCGATGGATGTGGATACCCGAGGGCCAAACAGGGGAAAGAG 60

QY 61 CGCTTGTGAATGTGAAAAAATGGTAATGGCAATTGGCCTCTGGGCCATTGGTAT 120  
 Db 61 CGCTTGTGAATGTGAAAAAATGGTAATGGCAATTGGCCTCTGGGCCATTGGTAT 120

QY 121 AACGTGGCATCTGGAGGACCATTTAGGATCTTGATAGATGTAAGTAACTACAG 180  
 Db 121 AACGTGGCATCTGGAGGACCATTTAGGATCTTGATAGATGTAAGTAACTACAG 180

QY 181 GCGTCGGTACTCTGAGAAGTGTACTGTGCAATGGAGCTCTGAACCATGTTAAC 240  
 Db 181 GCGTCGGTACTCTGAGAAGTGTACTGTGCAATGGAGCTCTGAACCATGTTAAC 240

QY 241 TTCCACTGCAATCTCTCGGGCTAACAAACAGCACAGGTGTCCATTGGACAGAG 300  
 Db 241 TTCCACTGCAATCTCTCGGGCTAACAAACAGCACAGGTGTCCATTGGACAGAG 300

QY 301 TGGAAATCCAATGTTGGCACTAG 327  
 Db 301 TGGAAATCCAATGTTGGCACTAG 327

XX Human secreted protein 5' EST, SEQ ID NO: 3894.

XX Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;

XX gene therapy; chromosome mapping; ss.

XX Homo sapiens.

XX EP1033401-A2.

XX 06-SEP-2000.

XX 21-FEB-2000; 2000EP-00200610.

XX 26-FEB-1999; 99US-0122487P.

XX (GBEST ) GENSET.

XX Dumas Milne Edwards J, Ducleir A, Giordano J;

XX PN WO2004060270-A2.

XX DR 22-JUL-2004.

XX DR P-PSDB; AAG03890.

XX DR 15-OCT-2003; 2003WO-US029126.

PT	New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.
PT	Claim 1; SEQ ID NO 3894; 71pp + Sequence Listing; English.
XX	The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. An ORF has been identified within the sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are therefore used to obtain full length mRNAs with intact 5' ends and can therefore be used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors
XX	Sequence 482 BP; 116 A; 103 C; 121 G; 140 T; 0 U; 2 Other;
XX	Query Match 100.0%; Score 327; DB 3; Length 482;
XX	Best Local Similarity 100.0%; Pred. No. 2.6e-157;
XX	Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 ATGGCGCCAGCGATGGATGTGGATACCCGAGGGCACCAACCGGGCCAGAG 60
Db	1 ATGGCGCCAGCGATGGATGTGGATACCCGAGGGCACCAACAGGGCAAGAG 60
QY	61 CGCTTGTGAATGTGAAAAAATGGTAATGGCAATTGGCCTCTGGGCCATTGGTAT 120
Db	61 CGCTTGTGAATGTGAAAAAATGGTAATGGCAATTGGCCTCTGGGCCATTGGTAT 120
QY	121 AACGTGGCATCTGGAGGACCATTTAGGATCTTGATAGATGTAAGTAACTACAG 180
Db	121 AACGTGGCATCTGGAGGACCATTTAGGATCTTGATAGATGTAAGTAACTACAG 180
QY	181 GCGTCGGTACTCTGAGAAGTGTACTGTGCAATGGAGCTCTGAACCATGTTAAC 240
Db	181 GCGTCGGTACTCTGAGAAGTGTACTGTGCAATGGAGCTCTGAACCATGTTAAC 240
QY	241 TTCCACTGCAATCTCTCGGGCTAACAAACAGCACAGGTGTCCATTGGACAGAG 300
Db	241 TTCCACTGCAATCTCTCGGGCTAACAAACAGCACAGGTGTCCATTGGACAGAG 300
QY	301 TGGAAATCCAATGTTGGCACTAG 327
Db	301 TGGAAATCCAATGTTGGCACTAG 327
XX	RESULT 2
ID	AA03896 standard; cDNA; 482 BP.
XX	Human secreted protein 5' EST, SEQ ID NO: 3894.
XX	Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX	gene therapy; chromosome mapping; ss.
XX	Homo sapiens.
XX	EP1033401-A2.
XX	06-OCT-2000 (first entry)
XX	Human secreted protein 5' EST, SEQ ID NO: 3894.
XX	Human tumour-associated antigenic target (TAT) cDNA sequence #4374.
XX	human; tumour-associated antigenic target; TAT; cytosatic; gene therapy;
XX	cancer; cell proliferative disorder; gene; ss.
OS	Homo sapiens.
XX	ADQB7496;
AC	ADQB7496;
XX	07-OCT-2004 (first entry)
XX	Human tumour-associated antigenic target (TAT) cDNA sequence #4374.
DB	Human tumour-associated antigenic target; TAT; cytosatic; gene therapy;
XX	KW human; tumour-associated antigenic target; TAT; cytosatic; gene therapy;
XX	cancer; cell proliferative disorder; gene; ss.
OS	Homo sapiens.
XX	WO2004060270-A2.
XX	PN WO2004060270-A2.
XX	DR 22-JUL-2004.
XX	P-PSDB; AAG03890.
XX	DR 15-OCT-2003; 2003WO-US029126.







molecule which binds to a TAT polypeptide; fusion proteins comprising a TAT polypeptide; and methods and compositions for the treatment or diagnosis of cancer in mammals. TAT polypeptides, nucleic acids, antibodies, antagonists, binding molecules and compositions are useful for diagnosing or treating a cell proliferative disorder associated with increased TAT expression, particularly cancers such as breast cancer, colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder cancer, pancreatic cancer, cervical cancer, cancers of the central nervous system, melanoma and leukaemia. TAT nucleic acids may further be used as hybridisation probes, in chromosome and gene mapping, in chromosome identification and in gene therapy. The present sequence represents a TAT nucleic acid of the invention.

Sequence 508 BP; 126 A; 106 C; 124 G; 152 T; 0 U; 0 Other;

Query Match 100.0%; Score 327; DB 13; Length 508;

Best Local Similarity 100.0%; Pred. No. 2 6e-157;

Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC 1 ATGGCGGAGCGTGTGGATACCCGGAGGGCACCAACAGGGCGGGCAAGAAG 60

Db 7 ATGGGGCAGCGATGGATGTGGATACCCGGAGGGCACCAACAGGGCGGGCAAGAAG 66

Qy 61 CGCTTTGAACTGTGAAAGGNGGAATGGCAGTAGGCCCTCTGGCCCTGGGATATTGGGTGAT 120

Db 67 CGCTTTGAACTGTGAAAGGNGGAATGGCAGTAGGCCCTCTGGCCCTGGGATATTGGGTGAT 126

Qy 121 AACCTGGCATCTGGAGGACCATTTGGCATAGATGTAAGGTAAACCAAG 180

Db 127 AACCTGTGCCATCTGGAGGACCATTTGGCATAGATGTAAGGTAAACCAAG 186

Qy 181 GCGTCCGGCTACTTCAGAAGAGTGTACTGTCGATGGGAGTCGTCGTAACCATGCTTTCAC 240

Db 187 GCGTCCGGCTACTTCAGAAGAGTGTACTGTCGATGGGAGTCGTCGTAACCATGCTTTCAC 246

Qy 241 TTCCCACTGATCTCTCGCTGGCTCAAACACAGAACAGAGAG 300

Db 247 TTCCCACTGATCTCTCGCTGGCTCAAACACAGAACAGGTGTGTCGTCGTAACAGAGAG 306

Qy 301 TGGGATTCAAAAGATGGCACTAG 327

Db 307 TGGGATTCAAAAGATGGCACTAG 333

RESULT 8  
ACH29979 standard; CDNA; 476 BP.

XX AC ACH29979;

XX DT 13-OCT-2003 (first entry)

XX DE Human testis CDNA #365.

XX KW Human; **ss**; sequencing by hybridisation; SBH; expressed sequence tag; EST;

KW genome mapping; biodiversity; genetic disorder.

XX Homo sapiens.

XX US2003073623-A1.

XX PD 17-APR-2003.

XX PF 30-JUL-2001; 2001US-00918995.

XX PR 30-JUL-2001; 2001US-00918995.

XX PA (DRMANAC R T.

PA (LABA) LABAT I.

PA (STAC) STACHE-CRAIN B.

PA (DICK) DICKSON M C.

PA (JONE) JONES L W.

PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;  
XX WP; 2003-615964/58.

PT New polynucleotide sequences obtained from various cDNA libraries, useful for hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA.

XX Claim 1; SEQ ID NO 17191; 44pp; English.

XX The invention relates to an isolated polynucleotide comprising any one of CC 3843 cDNA sequences, appearing as ACH12789-Ach50831, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences CC are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, CC in forensics, in assessing biodiversity, or in identifying mutations responsible for genetic disorders and other traits. The nucleotide CC sequences are also useful as hybridisation probes, as oligomers for PCR, CC for chromosome and gene mapping, in the recombinant production of CC protein, or in generating antisense DNA or RNA. The purified polypeptide CC is useful for generating antibodies specific for it. The present sequence CC is one of the 3803 isolated cDNA/EST sequences. Note: The sequence data CC for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPRO at CC sedata.usptc.gov/sequence.html?docID=2003073623

XX Sequence 476 BP; 119 A; 111 C; 124 G; 118 T; 0 U; 4 Other;

Query Match 99.4%; Score 325; DB 9; Length 476;

Best Local Similarity 100.0%; Pred. No. 2.7e-156; Mismatches 0; Indels 0; Gaps 0;

CC Matches 325; Conservative 0; Mismatches 0;

CC CC 3 GGC GGCGGAGTGGATGTGGATACCCGGAGGGCACCAACAGGGCGGGCAAGAAGGCC 62

Db 74 GGC GGCGGAGTGGATGTGGATACCCGGAGGGCACCAACAGGGCGGGCAAGAAGGCC 133

Qy 63 CTGGAACTGAAAGATGGAAATGGAGTGCCATGGGAGTCGATTTGGGTGATAA 122

Db 134 CTGGAACTGAAAGATGGAAATGGAGTAGGCCCTGTGGGATATGGGTGATAA 193

Db 123 CTG GCC CATCTGGAGGAACCAATATGGATCTTTGGATAGAATGTAAGCTAACAGGGC 182

Db 194 CTGGCCATCTGGGGACCAATATGGATCTTTGGATAGTCAAGCTAACAGGGC 253

Qy 183 GTC CGC TACTTCAGAAGAGTGTACTGTCGATCGGGAGTGCTGTACCATGCTTCACTT 242

Db 254 GTC CGC TACTTCAGAAGAGTGTACTGTCGATCGGGAGTGCTGTACCATGCTTCACTT 313

Qy 303 GGA ATT CCA AAA AGT ATGGG GACTAG 327

Db 374 GGA ATT CCA AAA AGT ATGGG GACTAG 398

RESULT 9  
ADS09913/C  
ID ADS09913 standard; DNA; 3726 BP.

XX AC ADS09913;

XX DT 16-DEC-2004 (first entry)

XX Human therapeutic DNA - SEQ ID 150.

XX antiinflammatory; neuroprotective; antianaemic; cytostatic; vulnerary; inflammatory; haemoptysis; immunity; neurodegenerative; stem cell; aplastic anaemia; cancer; wound healing; gene therapy; ds; gene.

XX DT 02-DEC-2004 (first entry)  
 XX DE Breast cancer related marker, seq id 11311.  
 XX DE  
 XX KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.  
 XX KW  
 XX OS Homo sapiens.  
 XX OS  
 XX PN US2003099974-A1.  
 XX PN  
 XX PR 02-OCT-2002; 2002US-0416186P.  
 XX PR  
 XX PD 29-MAY-2003.  
 XX PD  
 XX PA (NUVE-) NUVELO INC.  
 XX PA  
 XX PI Tang YT, Asundi V, Ren F, Zhang J, Wehrman T, Wang Z, Ma Y, Weng G, Zhou P; DR 2004 668857/65.  
 XX DR  
 XX P-PSDB; ADS10557.  
 XX PT New polynucleotide, useful in preparing a composition for diagnosing or treating inflammatory, neurodegenerative or stem cell disorders, e.g., aplastic anemia or cancer for promoting wound healing.  
 XX PT  
 XX PS SEQ ID NO 150; 718pp; English.  
 XX PS  
 CC The invention relates to a novel isolated polynucleotide and the encoded polypeptide. The molecules of the invention demonstrate antiinflammatory, neuroprotective, antianemic, cytostatic and vulnerary activities and may be useful in preparing a composition for diagnosing or treating inflammatory, haematopoietic, immune, neurodegenerative or stem cell disorders, such as aplastic anaemia or cancer, as well as for promoting wound healing. The molecules may also be utilised during gene therapy procedures. The current sequence is that of a human therapeutic DNA of the invention. The current sequence is not shown explicitly within the specification but can be accessed from the WIPO web-site.  
 XX SQ Sequence 3726 BP; 996 A; 955 C; 845 G; 930 T; 0 U; 0 Other;  
 XX SQ  
 CC Query Match 98.2%; Score 321; DB 13; Length 3726;  
 CC Best Local Similarity 100.0%; Pred. No. 2 9e-154; Indels 0; Gaps 0;  
 CC Matches 321; Conservative 0; Mismatches 0; U; 0 Other;  
 CC SQ  
 CC Query 7 GCAGCGATGGATGTTGATACCCGAGCGGCCACCAACAGCGGCCGAAAGAAGCGCTT 66  
 CC DB 492 GCAGCGATGGATGTTGATACCCGAGCGGCCACCAACAGCGGCCGAAAGAAGCGCTT 433  
 CC DB  
 CC Query 67 GAAGTGAAAAGTGGAAATGGAGTAGCCCTGTGGCCTGGGATATTGTTGATAACTGT 126  
 CC DB 432 GAAGTGAAAAGTGGAAATGGAGTAGCCCTGTGGCCTGGGATATTGTTGATAACTGT 373  
 CC DB  
 CC Query 127 GCCATCTGAGGAAACCAACATTGGATTTGCATAAGAATGTCAGTAACAGCTAACAGGGTTC 186  
 CC DB 372 GCCATCTGAGGAAACCAACATTGGATTTGCATAAGAATGTCAGTAACAGCTAACAGGGTTC 313  
 CC DB  
 CC Query 187 GCTACTTCAAGAGTGTACTGTGCACTGGGAACTCTGTAACCATGCTTTCACTTCAC 246  
 CC DB 312 GCTACTTCAAGAGTGTACTGTGCACTGGGAACTCTGTAACCATGCTTTCACTTCAC 253  
 CC DB  
 CC Query 247 TGCATCTCTGGCTGGCTCAAACACGACAGCTGGTGTCAATTGGACAACAGAGTGGAA 306  
 CC DB 252 TGCATCTCTGGCTGGCTCAAACACGACAGCTGGTGTCAATTGGACAACAGAGTGGAA 193  
 CC DB  
 CC Query 307 TTCCAAAAGTATGGGCACTAG 327  
 CC DB  
 CC Query 192 TTCCAAAAGTATGGGCACTAG 172  
 CC DB  
 CC Query 307 TTCCAAAAGTATGGGCACTAG 327  
 CC DB  
 CC Query 785 TTCCAAAAGTATGGGCACTAG 765  
 CC DB  
 RESULT 10  
 ACN90161/c  
 ID ACN90161 standard; DNA; 4543 BP.  
 XX  
 AC ACN90161;  
 XX  
 RESULT 11

ADQ92179 ID ADQ92179 standard; DNA; 503 BP. XX AC ADQ92179; XX DT 07-OCT-2004 (first entry) XX DE Human autoantigen DNA fragment MPMgp800L05536. XX ds; autoantigen; antibody; biosensor chip; extracorporeal differential diagnosis; autoimmune disease; ribosomal protein; tubulin; dolichyl-diphospho-oligosaccharide-glycosyl transferase; multiple sclerosis; rheumatoid arthritis; epitope mapping; affinity chromatography; electrophoresis; autoantibody apheresis; RNA interference; RNAi. XX OS Homo sapiens. XX PN WO2004058972-A1. XX PD 15-JUL-2004. XX PP 23-DEC-2002; 2002WO-EP014731. XX PR 23-DEC-2002; 2002WO-EP014731. XX PA (THIE) THIESSEN H. PA (LORE) LORENZ P. XX PT Thiesen H., Lorenz P.; DR WPI; 2004-543459/52. XX PT New human DNA autoantigens, useful as assay, diagnostic, and prognostic reagents and for treating autoimmune disease, also related expression products and antibodies with similar uses. XX PS Claim 1; SEQ ID NO 160; 110pp; German. XX CC This invention describes novel human DNA autoantigens which are used to CC produce recombinant expression vectors; prokaryotic or eukaryotic cells; CC poly- or mono-clonal antibodies (Ab) specific; hybridomas that express CC monoclonal Ab; biosensor chips having an addressable sequence pattern as CC medical or diagnostic instruments that include the biosensor; for CC extracorporeal differential diagnosis of autoimmune diseases and CC predisposition to them. The autoantigen polynucleotides encode ribosomal CC proteins; tubulins; dolichyl-diphospho-oligosaccharide-glycosyl CC transferases and proteins. The antibodies may be labelled conventionally CC with radioisotopes, coloured or fluorescent groups, or a member of the CC biocinavidin pair, or colloidal gold. The autoantigens can be directed CC against mitochondria, liver-kidney microsomes; histidyl-t-RNA; nuclear CC membrane; neutrophilic cytoplasm; insect cells; epidermal intracellular CC or basal membrane antigens; Golgi or cell nuclei, or associated with CC multiple sclerosis or rheumatoid arthritis. They are useful for epitope CC mapping; in affinity chromatography or electrophoresis; for diagnosis, CC diseases, particularly in vitro differential diagnosis of autoimmune CC diseases; to produce biosensor chips or for autoantibody apheresis. CC Autoantigen DNA can be used for therapeutic RNA interference against CC autoantibodies. Biochips that carry the new materials are useful in CC medical and diagnostic instruments. ADQ92020-ADQ92280 represent human CC autoantigens. XX SQ Sequence 503 BP; 131 A; 102 C; 120 G; 150 T; 0 U; 0 Other; Query Match 97.9%; Score 320; DB 12; Length 503; Best Local Similarity 100.0%; Pred. No. 1e-153; Indels 0; Gaps 0; Matches 320; Conservative 0; Mismatches 0; Gaps 0; QY 8 CAGCGATGGATGTGGATACCCGAGGCCAACGGCAAGGAAGGGCTTG 67 db 1 CAGCGATGGATGTGGATACCCGAGGCCAACGGCAAGGAAGGGCTTG 60	QY 68 AAGTAAAAAGTCGAATCAGTAGCCCTGGGACTGGCATATTGGTTGATAACTCTG 127 Db 61 AACGTAAAAGTCGAATCAGTAGGCCCTGGGACTGGCATATTGGTTGATACTCTG 120 QY 128 CCATCTGCAGGAACACATTATGGATCCTTGCATAGAATGTCAAAGCTTAACCGGGTCGG 187 Db 121 CCATCTGCAGGAACACATTATGGATCCTTGCATAGAATGTCAAACCGGGTCGG 180 QY 188 CTACTTCAGAAGAGGTGACTGTGCACTGGGACTGTGTAACCATGCTTTTCACTCCACT 247 Db 181 CTACTTCAGAAGAGGTGACTGTGCACTGGGACTGTGTAACCATGCTTTTCACTCCACT 240 QY 248 GCATCTCNGCNGCTCAAACAGCACAGGTGTCATTGGACAACAGAGACTGGGAT 307 Db 241 GCATCTCNGCNGCTCAAACAGCACAGGTGTCATTGGACAACAGAGACTGGGAT 300 QY 308 TCCA AAAACTATGGCACTAG 327 Db 301 TCCA AAAACTATGGCACTAG 320
RESULT 12 ABV25615/C ID ABV25615 standard; cDNA; 4476 BP. XX AC ABV25615; XX DT 16-SEP-2002 (first entry) XX DB Human prostate expression marker cDNA 25606. XX KW Human; prostate cancer; cytostatic; carcinogen; pharmacodynamic marker; KW pharmacogenomic marker; gene; ss. OS Homo sapiens. XX PN WO2001608860-A2. XX PD 23-AUG-2001. XX PR 20-FEB-2001; 2001WO-US005171. XX PR 17-FEB-2000; 2000US-0183319P. PR 16-MAR-2000; 2000US-0189862P. PR 25-MAY-2000; 2000US-0207454P. PR 09-JUN-2000; 2000US-0211314P. PR 18-JUL-2000; 2000US-0219007P. PR 13-DEC-2000; 2000US-0255281D.	XX Schlegel R, Endege WO, Monahan JE; WPI; 2001-662795/76. XX PT Novel isolated nucleic acid molecule associated with cancerous state of PT prostate cells and correlating with presence of prostate cancer, useful PT for detecting presence of prostate cancer, stage of prostate cancer. XX Claim 1; Page 5119-5120; 11750pp; English. XX (MLL-) MILLENNIUM PREDICTIVE MEDICINE INC. XX PA (MLL-) MILLENNIUM PREDICTIVE MEDICINE INC. XX CC a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the CC specification or its complement. (I) is useful for: (a) assessing whether CC a patient is afflicted with prostate cancer; (b) monitoring the CC progression of prostate cancer in a patient; (c) assessing the efficacy CC of a test compound to inhibit prostate cancer in a patient; (d) assessing CC the efficacy of a therapy for inhibiting prostate cancer in a patient; CC (e) selecting a composition for inhibiting prostate cancer in a patient; CC (f) assessing the prostate cell carcinogenic potential of a compound; (g) CC determining whether prostate cancer has metastasized in a patient; (h) CC assessing the aggressiveness or indolence of prostate cancer in a patient

CC ; (I) is also useful as a pharmacodynamic or pharmacogenomic marker  
 XX Sequence 4476 BP; 1085 A; 1129 C; 1015 G; 1247 T; 0 U; 0 Other;  
 SQ Query Match 94.2%; Score 308; DB 5; Length 4476;  
 Best Local Similarity 100.0%; Pred. No. 1-4e-147;  
 Matches 308; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCAGCGATGGATGTTGCAACCCGAGGGACCCACAGGGCGGGCAAAGGGCTT 66  
 Db 1014 GCAGCGATGGATGGTGAATCCCGAGGGACCCACAGGGCGGGCAAAGGGCTT 955  
 Qy 67 GAAGTGAAGAAAGTGGAAATGGAGTAGCCTCTGGGCTGGSATATGTGGTTGATAACTGT 126  
 Db 954 GAAGTGAAGAAAGTGGAAATGGAGTAGCCTCTGGGCTGGSATATGTGGTTGATAACTGT 895  
 Qy 127 GCCATCTGCAGGAACCAATTGGATCTTGATAGAATGTCAGCTAACAGGGTCC 186  
 Db 894 GCCATCTGCAGGAACCAATTGGATCTTGATAGAATGTCAGCTAACAGGGTCC 835  
 Qy 187 GCTACTTCAGAAGAGTGTACTGTGCCATGGGAATGCTGTAAACCATGCTTTCACTTCAC 246  
 Db 834 GCTACTTCAGAAGAGTGTACTGTGCCATGGGAATGCTGTAAACCATGCTTTCACTTCAC 775  
 Qy 247 TGCAATCTCGCTGGCTCAAAACAGACAAGAGTGGGA 306  
 Db 715 TGCAATCTCGCTGGCTCAAAACAGACAAGAGTGGGA 715  
 Qy 307 TTCCAAA 314  
 Db 714 TTCCAAA 707

RESULT 13  
 ACL57420 ID ACL57420 standard; cDNA; 311 BP.  
 AC ACL57420;  
 XX DT 24-MAR-2005 (first entry)  
 DE Human colon cancer differentially expressed polynucleotide, SEQ ID:3555.  
 XX KW Differential expression; diagnosis; therapy; drug screening; cancer;  
 neoplasm; colon tumor; breast tumor; pancreas tumor; cytostatic; vaccine;  
 SS .  
 KW Homo sapiens.  
 OS PN WO2005000087-A2.  
 XX PD 06-JAN-2005.  
 PF 13-MAY-2004; 2004WO-US015421.  
 XX PR 03-JUN-2003; 2003US-0475872P.  
 XX PA (CHIR ) CHIRON CORP.  
 PI Randazzo F, Moler E, Escobedo J, Garcia PD;  
 XX DR WPI; 2005-075421/08.  
 XX PT New isolated polynucleotides, which are differentially expressed in colon  
 PR cancer cell, useful for treating cancer, e.g. colon cancer, breast  
 PR cancer, or pancreatic cancer.  
 XX PS Claim 1; SEQ ID NO 3555; 97pp; English.

CC The invention relates to 9672 polynucleotides (ACL53866 -ACL63337) which  
 CC are differentially expressed in colon cancer cells. The invention also  
 CC relates to vectors and host cells comprising a differentially expressed  
 CC polynucleotide of the invention; a method for detecting a cancerous cell

CC by detection of a gene product of the polynucleotides; a method for  
 CC inhibiting a cancerous phenotype of a cell by inhibiting a gene product  
 CC of the polynucleotides; a method of treating an individual with cancer by  
 CC administration of a modulator of a gene product of the polynucleotides;  
 CC and an isolated antibody that specifically binds to a polypeptide encoded  
 CC by one of the 9672 polynucleotides. The polynucleotides, polypeptides,  
 CC antibodies, and methods are useful for the detection of cancerous cells;  
 CC identification of agents that modulate the phenotype of cancerous cells;  
 CC for the identification of therapeutic targets for cancer chemotherapy;  
 CC and for the treatment of cancer, especially colon cancer and metastases  
 CC colon cancer, but also breast or pancreatic cancer. The polynucleotides  
 CC are also useful as source of probes or primers for use in diagnostic  
 CC methods. The differentially expressed polynucleotides or their encoded  
 CC proteins can additionally be used as vaccines to modulate primary immune  
 CC responses for the prevention or treatment of cancer. The present sequence  
 CC represents a specifically claimed polynucleotide which is differentially  
 CC expressed in colon cancer. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX SQ Sequence 311 BP; 77 A; 75 C; 87 G; 72 T; 0 U; 0 Other;  
 Query Match 90.5%; Score 296; DB 14; Length 311;  
 Best Local Similarity 100.0%; Pred. No. 2.1-e-141;  
 Matches 296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ATGGCGAGCGATGGATGTGATACCCGGAGGGCACCACAGGGCGGGCAAAGAAG 60  
 Db 16 ATGGCGAGCGATGGATGTGATGGATACCCGGAGGGCACCACAGGGCGGGCAAAGAAG 75  
 Qy 61 CGCTTGAACTGAAAAAGTGGAAATGCACTAGCTGGCCCTCTGGGATATTGGTTGTAT 120  
 Db 76 CGCTTGAACTGAAAAAGTGGAAATGCACTAGCTGGCCCTCTGGGATATTGGTTGTAT 135  
 Qy 121 AACGTGCGCATCTCGAGGACCAATTGGATCTTGATAGAATGTCAGCTAACGAC 180  
 Db 136 AACGTGCGCATCTCGAGGACCAATTGGATCTTGATAGAATGTCAGCTAACGAC 195  
 Qy 181 GCGTCGCTACTTCTGAGAGTGTACTGTGCACTGGGGACTCTGTAACCATGCTTCAC 240  
 Db 196 GCGTCGCTACTTCTGAGAGTGTACTGTGCACTGGGGACTCTGTAACCATGCTTCAC 255  
 Qy 241 TTCCACTGCACTCTCGCTGGCTAAAACAGCACAGGTGTGTCATTGGACAAACAG 296  
 Db 256 TTCCACTGCACTCTCGCTGGCTAAAACAGCACAGGTGTGTCATTGGACAAACAG 311

RESULT 14  
 ADF42703\_C  
 ID ADF42703 standard; cDNA; 3484 BP.  
 AC ADF42703;  
 XX DT 26-FEB-2004 (first entry)  
 XX DE Human Testicon-1 nucleotide sequence SEQ ID NO:9.  
 KW XX diabetic; pre-diabetic; Type 2 diabetes; antidiabetic; gene therapy;  
 KW diabetes; insulin resistance; metabolic disease; human; gene; ss.  
 XX OS Homo sapiens.  
 XX PN WO2003102163-A2.  
 XX PD 11-DEC-2003.  
 XX PR 04-JUN-2003; 2003WO-US017825.  
 XX PN 04-JUN-2002; 2002US-0385857P.  
 PR 04-JUN-2002; 2002US-0386013P.  
 PR 04-JUN-2002; 2002US-0386074P.

PR	04-JUN-2002; 2002US-0386107P.	Db	236 GAGGTGAAAAAGTGGAAATGCACTAGGCCCTCTGGGATATTGGTTGATAACTGT 177
PR	05-JUN-2002; 2002US-0386314P.	Qy	127 GCGATCTCAGGACCATTTATGCACTTTCGCTTGCAGTACATGCTACCGCGCTCC 186
PR	05-JUN-2002; 2002US-0386326P.	Db	176 GCGATCTCAGGACCATTTATGCACTTTCGCTTGCAGTACATGCTACCGCGCTCC 117
PR	05-JUN-2002; 2002US-0386332P.	Qy	187 GCTACTTCGAAAGTGTACTGTGCTATGGGAGTCGATGGGAGTCGTAACCTGCTTCCAC 246
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PR	06-JUN-2002; 2002US-0386955P.		
PR	06-JUN-2002; 2002US-0387017P.		
PR	06-JUN-2002; 2002US-0387026P.		
PR	20-JUN-2002; 2002US-0386865P.		
XX	(META-) METABOLEX INC.		
XX	Allan B, Gregoire F, Lavan B, Moodie S, Waters S, Wong C;		
PT	XX		
XX	WPI; 2004-053469/05.		
DR	P-PSDB; ADF42704.		
XX	Identifying an agent for treating diabetic or pre-diabetic individuals		
PR	PR comprises contacting an agent with a polypeptide, e.g., human ceramidase,		
PR	and selecting an agent that modulates the expression or activity of the		
PR	polypeptide.		
XX	Disclosure; SEQ ID NO 9; 209pp; English.		
XX	The present invention describes a method for identifying an agent for		
CC	treating a diabetic or pre-diabetic individual. The method comprises		
CC	contacting an agent to a mixture comprising a polypeptide encoded by a		
CC	nucleic acid that hybridises under stringent conditions to a nucleic acid		
CC	encoding any of the 23 fully defined amino acid sequences given in the		
CC	specification, and selecting an agent that modulates the expression or		
CC	activity of the polypeptide. Also described: (1) a method of treating a		
CC	diabetic or pre-diabetic animal, comprising administering to the animal a		
CC	therapeutic amount of an agent identified by the method described above;		
CC	(2) a method of introducing an expression cassette into a cell,		
CC	comprising introducing into the cell an expression cassette comprising a		
CC	promoter operably linked to a polynucleotide encoding a polypeptide,		
CC	where the polynucleotide hybridises under stringent conditions to a		
CC	nucleic acid encoding the above amino acid sequences; and (3) a method of		
CC	diagnosing detecting in a sample from the individual the level of a		
CC	polypeptide or the level of the above-mentioned polynucleotide encoding		
CC	the polypeptide, where a modulated level of the polypeptide or		
CC	polynucleotide in the sample compared to a level of the polypeptide or		
CC	polynucleotide in either a lean individual or a previous sample from the		
CC	individual indicates that the individual is diabetic or pre-diabetic. The		
CC	method is useful in diagnosing and treating diabetes, insulin resistance		
CC	or related metabolic diseases in human subjects. The method may also be		
CC	used in identifying agents for treating diabetic or pre-diabetic		
CC	individuals. The present sequence is used in the exemplification of the		
CC	present invention.		
XX	Sequence 3484 BP; 894 A; 910 C; 808 G; 872 T; 0 U; 0 Other;		
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Db	296	GCAGGGATGGATGTGGATAACCCGAGGGACCCAAAGCGGCCAGAACAGAAGGCC	TTT 237
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QY	127	GCCATCTGCAGGAACCA CATTATGGATCTTGCA TAGA AAGTCAGCTAACCGCGTCC	186
Db	176	GCCATCTGCAGGAACCA CATTATGGATCTTGCA TAGA AAGTCAGCTAACCGCGTCC	117
QY	187	GCTACTCAGAGAGTGACTGTGCA TGGGAGCTGTACCATGTTTCACTTCAC	TCCAC 246
Db	116	GCTACTCAGAGAGTGACTGTGCA TGGGAGCTGTACCATGTTTCACTTCAC	TCCAC 57
QY	247	TGCATCTCTCGCTGGCTAAAAACACCA CAGGTGTCACTGGACAA	CAGAGTG 302
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	CQ68451	6	CQ68451	CQ68451 Sequence
3	CQ63099	6	CQ63099	CQ63099 Sequence
4	CQ65007	6	CQ65007	CQ65007 Sequence
5	CQ712328	6	CQ712328	CQ712328 Sequence
6	CQ711142	6	CQ711142	CQ711142 Sequence
7	BD07641	6	BD07641	BD07641 Sequence
8	AX88031	6	AX88031	AX88031 Sequence
9	CQ729899	6	CQ729899	CQ729899 Sequence
10	BD211520	6	BD211520	BD211520 Von Hippel
11	AR640603	6	AR640603	AR640603 Sequence
12	AF10598	8	AF10598	AF10598 Homo sapi
13	CQ701366	6	CQ701366	CQ701366 Sequence
14	BC01466	8	BC01466	BC01466 Homo sapi
15	CR45650	8	CR45650	CR45650 Homo sapi
16	BC017370	6	BC017370	BC017370 Homo sapi
17	CQ82496	6	CQ82496	CQ82496 Sequence
18	HUMYQ60A05	8	HUMYQ60A05	HUMYQ60A05 Homo sapi

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed. and is derived by analysis of the total score distribution.

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4	327	100.0	467	6	CQ695007	Sequence
5	327	100.0	471	6	CQ712328	Sequence
6	327	100.0	472	6	CQ711142	Sequence
7	327	100.0	482	6	BD07641	Sequence
8	327	100.0	482	6	AX898031	Sequence
9	327	100.0	507	6	CQ79899	Sequence
10	327	100.0	508	6	BD21520	Von Hippel
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16	327	100.0	554	8	BC017370	Homo sapi
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VERSION	CQ698451.1 GI:42252856							
KEYWORDS								
SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;							
	Hominidae; Homo.							
REFERENCE	Liew, C.C., Marshall, W.E. and Zhang, H.							
AUTHORS	Compositions and methods relating to osteoarthritis							
TITLE								
JOURNAL	Patent: WO 02070737-A 43377 12-SEP-2002;							
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SOURCE	Homo sapiens (human)							
ORGANISM	Homo sapiens							
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;							
	Hominidae; Homo.							
REFERENCE	Liew, C.C., Marshall, W.E. and Zhang, H.							
AUTHORS	Compositions and methods relating to osteoarthritis							
TITLE								
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Qy	61 CGCTTGAAGTGAAAAGTGTGAATGGAGAACCATTTGGATCTGGATAAGCTGGTGTAT 120							
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RESULT 4								
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DEFINITION	Sequence 39933 from Patent WO02070737.							
VERSION	CQ695007.1 GI:42240530							
KEYWORDS								
SOURCE	Homo sapiens (human)							



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			JP 200126182-A/3887.		
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	ORGANISM				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.				
	REFERENCE				
	AUTHORS			Dumas Maine Edwards,J.B., Duclert,A. and Giordano,J.Y.	
	TITLE			Expressed sequence tags and encoded human proteins	
	JOURNAL			Patent : EP 1033401 A 1894 06-SEP-2000;	
	FEATURES			Genseq (FR) Location/Qualifiers	
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	Qy			181 GGCTCGGTACTCTGCGATGAGAGTGTACTGTGATGGGAGTTGTAACCATGCTTTCAC 240	
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	Qy			241 TTCCACTGTCATCTGCGATGGCTGGTCAAACACGACAGGTTGTCATTTGACAACAGAGAG 300	
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	Db			CQ729899 Version CQ729899	
	Qy			GI:42302243	
	Db			Homo sapiens (human)	
	Qy			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.	
	Db			REFERENCE 1	

**AUTHORS** Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.

**TITLE** Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof

**JOURNAL** Patent: WO 02068579-A 15833 06-SEP-2002;

**FEATURES** PE Corporation (NY) (US)

**source** Location/Qualifiers

1. 507  
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**DEFINITION** VonHippel-Lindau tumor suppressor complex and novel component of SCF ubiquitin ligase.

**ACCESSION** BD271520

**VERSION** BD271520\_1 GI:33081288

**KEYWORDS** JP 2003541775-A/1.

**SOURCE** Homo sapiens (human)

**ORGANISM** Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homidae; Homo

**REFERENCE** Conaway, J.W., Conaway, R.C. and Kamura, T.

**AUTHORS** VonHippel-Lindau tumor suppressor complex and novel component of SCF ubiquitin ligase

**TITLE** Patent: JP 2002541775-A 1 10-DEC-2002;

**JOURNAL** OKLAHOMA MEDICAL RESEARCH FOUNDATION

**COMMENT** OS Homo sapiens (human)  
 PN JP 2003541775-A/1  
 PD 10-DEC-2002  
 PP 25-FEB-2000 JP 2000601023  
 PR 26-FEB-1999 US 60121787  
 PI JOAN W CONAWAY, RONALD C CONAWAY, TAKUMI KAMURA PC  
 C12N1/09, A61K38/00, A61K38/53, A61K45/00, A61P35/00, C07K14/47, PC  
 C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N9/00, C12P21/02, G01N33/15, G01N33/ PC  
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**CC** VonHippel-Lindau tumor suppressor complex and novel component of SCF ubiquitin ligase

**CC** Key Location/Qualifiers

**CC** Source 1. 508 /organism="Homo sapiens" Location/Qualifiers

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  Qy 241 TTCCACTGCATCTCTGCTGCTCAAACAGCACGGTGCTCATTGGACAAGAG 300
  Db 247 TTCCACTGCATCTCTGCTGCTCAAACAGCACGGTGCTCATTGGACAAGAG 306
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  Db 307 TGGGATTCCAAAAGTAGTGGCCACTAG 333

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**RESULT** 11

**AR640603** AR640603 508 bp DNA linear PAT 20-APR-2005

**LOCUS** AR640603 Sequence 3 from patent US 6858709.

**DEFINITION** Component of von Hippel-Lindau tumor suppressor complex and SCF ubiquitin ligase

**ACCESSION** AR640603 Version AR640603.1 GI:62775412

**KEYWORDS** Unknown

**SOURCE** Unknown

**ORGANISM** Unclassified

**REFERENCE** (bases 1 to 508) Conway, J.W., Conway, R.C. and Kamura, T.

**AUTHORS** Conway, J.W., Conway, R.C. and Kamura, T.

**TITLE** Component of von Hippel-Lindau tumor suppressor complex and SCF ubiquitin ligase

**JOURNAL** Patent: US 6858709-A 3 22-FEB-2005;

**FEATURES** 1. 508 /organism="unknown" /mol\_type="genomic DNA"

**ORIGIN**

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Query Match 100.0%; Score 327; DB 6; Length 508;
Best Local Similarity 100.0%; Pred. No. 3..6..-184;
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REFERENCE				REFERENCE	1	Liew, C.C., Marshall, W.E. and Zhang, H.	
AUTHORS	Kamura, T., Koepf, D.M., Conrad, M.N., Skowyra, D., Moreland, R.J., Iliopoulos, O., Lane, W.S., Kaelin, W.G. Jr., Eledge, S.J., Conaway, R.C., Harper, J.W. and Conaway, J.W.			AUTHORS	1	Compositions and methods relating to osteoarthritis	
TITLE	Rbx1, a component of the VHL tumor suppressor complex and SCF ubiquitin ligase			TITLE	1	Patent: WO 0207373-A 46292 12-SEP-2002;	
JOURNAL	Science 284 (5414), 657-661 (1999)			JOURNAL	1	Chondrogenic Inc. (CA)	
PUBLMED	10213631			FEATURES	1	Location/Qualifiers	
REFERENCE	2 (bases 1 to 508)			FEATURES	1	Source	
AUTHORS	Kamur, T., Lane, W.S., Conaway, R.C. and Conaway, J.W.			FEATURES	1	Query Match	100.0%; Score 327; DB 6; Length 523;
TITLE	Direct Submission			FEATURES	1	Best Local Similarity	100.0%; Pred. No. 3..e-184; Mismatches 0; Indels 0; Gaps 0;
JOURNAL	Submitted (05-APR-1999) Prog. Molec. Cell Biol., HHMI, Oklahoma			FEATURES	1	Matches	327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db AUTHORS Woessner,J., Tan,F., Marra,M., Kucaba,T., Yandell,M., Martin,J., Bowers,Y., Steptoe,M., Theising,B., Marth,G., Bowles,L., Wylie,T., Underwood,K., Chappell,J., Person,B., Geisei,S., Allen,M., Harvey,N., Papo,D., Chamberlain,A., Morales,R., Schubk,R., Ritter,E., Kohn,S., Swaller,T., Behymer,K., Hillier,L., Wilson,R. and Waterston,R.	248	GCATCTCTCTGGATGGGAGTCTGTAAACCATGCTTC	307
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Db AUTHOR TITLE Direct Submission	248	GCATCTCTCTGGATGGGAGTCTGTAAACCATGCTTC	307
Db COMMENT Submitted (24-Aug-1998) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA	248	GCATCTCTCTGGATGGGAGTCTGTAAACCATGCTTC	307
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REFERENCE REFERENCES	248	GCATCTCTCTGGATGGGAGTCTGTAAACCATGCTTC	307
AUTHORS Thiesen,H.J. and Lorenz,P.	248	GCATCTCTCTGGATGGGAGTCTGTAAACCATGCTTC	307
JOURNAL Human autoantigenic and use thereof	248	GCATCTCTCTGGATGGGAGTCTGTAAACCATGCTTC	307
PATENT: WO2004058972-A 160 15-JUL-2004; Thiesen, Hans-Juergen (DE); Lorenz, Peter (DE)	248	GCATCTCTCTGGATGGGAGTCTGTAAACCATGCTTC	307
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**ORIGIN**

Query Match	90.5%	Score 296; DB 8; Length 3484;	Score 275; DB 8; Length 306;
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominidae; Homo.

REFERENCE AY099360  
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.  
TITLE Compositions and methods relating to osteoarthritis  
JOURNAL Patent: WO 02070737-A 47656 12-SEP-2002;  
Chondrogen Inc. (CA)

FEATURES Source  
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**ORIGIN**

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REFERENCE	1.	Shiffman, D., Somogyi, R., Lawn, R., Seilhamer, J.J., Porter, G.J., Mikita, T. and Tai, J.	Genes expressed in foam cell differentiation						
AUTHORS	Shiffman, D., Somogyi, R., Lawn, R., Seilhamer, J.J., Porter, G.J., Mikita, T. and Tai, J.	Patent: WO 0177389-A 99 18-OCT-2001;	Incyte Genomics, Inc. (US)	Location/Qualifiers	1..5347	/organism="Homo sapiens"	/mol_type="unassigned DNA"	/db_xref="taxon:606"	
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Qy	139	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	198						
Db	2836	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	2895						
ORIGIN									
Query Match	76.1%	Score 249; DB 6; Length 3208;							
Best Local Similarity	100.0%	Pred. No. 2.6e-137;							
Matches	249;	Conservative 0; Mismatches 0;	Indels 0;	Gaps 0;					
Qy	79	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	138						
Db	2776	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	2835						
Qy	139	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	198						
Db	2836	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	2895						
ORIGIN									
Query Match	76.1%	Score 249; DB 6; Length 3208;							
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Qy	79	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	138						
Db	2776	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	2835						
Qy	139	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	198						
Db	2836	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	2895						
ORIGIN									
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Best Local Similarity	100.0%	Pred. No. 2.6e-137;							
Matches	249;	Conservative 0; Mismatches 0;	Indels 0;	Gaps 0;					
Qy	79	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	138						
Db	2776	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	2835						
Qy	139	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	198						
Db	2836	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	2895						
ORIGIN									
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Qy	79	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	138						
Db	2776	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	2835						
Qy	139	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	198						
Db	2836	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	2895						
ORIGIN									
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Matches	249;	Conservative 0; Mismatches 0;	Indels 0;	Gaps 0;					
Qy	79	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	138						
Db	2776	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	2835						
Qy	139	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	198						
Db	2836	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	2895						
ORIGIN									
Query Match	76.1%	Score 249; DB 6; Length 3208;							
Best Local Similarity	100.0%	Pred. No. 2.6e-137;							
Matches	249;	Conservative 0; Mismatches 0;	Indels 0;	Gaps 0;					
Qy	79	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	138						
Db	2776	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	2835						
Qy	139	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	198						
Db	2836	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	2895						
ORIGIN									
Query Match	76.1%	Score 249; DB 6; Length 3208;							
Best Local Similarity	100.0%	Pred. No. 2.6e-137;							
Matches	249;	Conservative 0; Mismatches 0;	Indels 0;	Gaps 0;					
Qy	79	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	138						
Db	2776	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	2835						
Qy	139	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	198						
Db	2836	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	2895						
ORIGIN									
Query Match	76.1%	Score 249; DB 6; Length 3208;							
Best Local Similarity	100.0%	Pred. No. 2.6e-137;							
Matches	249;	Conservative 0; Mismatches 0;	Indels 0;	Gaps 0;					
Qy	79	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	138						
Db	2776	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	2835						
Qy	139	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	198						
Db	2836	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	2895						
ORIGIN									
Query Match	76.1%	Score 249; DB 6; Length 3208;							
Best Local Similarity	100.0%	Pred. No. 2.6e-137;							
Matches	249;	Conservative 0; Mismatches 0;	Indels 0;	Gaps 0;					
Qy	79	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	138						
Db	2776	TGGATGCACTGGATGGGAGTCAGTCACTTCTGGCTGGATAATCTGGCTACTCTGCAGG	2835						
Qy	139	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	198						
Db	2836	AACACATTATGGATCTTGCATAAGTCAAGCTAACGGGTCGGCTACTCTGCAGG	2895						
ORIGIN									
Query Match	76.1%	Score 249; DB 6; Length 3208;							
Best Local Similarity	100.0%</								

RESULT 26	Qy	Query Match	76.1%	Score 249;	DB 6;	Length 3208;
AR651451	Qy	Best Local Similarity 100.0%;	Pred. No. 2.6e-137;	Mismatches 0;	Indels 0;	Gaps 0;
LOCUS	Qy	Matches 249; Conservative 0;	Mismatches 0;	Indels 0;		
DEFINITION AR651451	Db	Sequence 27 from patent US 6881563.	DNA	linear	PAT 20-APR-2005	
VERSION AR651451.1	Db	3208 bp				
KEYWORDS Unknown.	Db	2776 TGGATGCGATGCCCTCGGCCCTGGGATATTGGTGTGATACTGTGCATCTCGC	138			
ORGANISM Unspecified.	Db	139 AACCAATTATGGATCTTCATAGAATGTCAAAGCTAACAGGCTCGGTACTTCAGAA	198			
REFERENCE 1 (bases 1 to 3208)	Db	2836 AACACATATGGATCTTCATAGAATGTCAAAGCTAACAGGCTCGGTACTTCAGAA	2895			
AUTHORS Donoho,G., Scoville,J., Turner,C.A. Jr., Friedrich,G., Abuin,A.,	Qy	199 GAGGTACGTGCGATGGGAGTCATGGTGTGATAACCCTTCATCTGTTTACACTGCTCGC	258			
Zambrowicz,B. and Sands,A.T.	Db	2896 GAGTGTACGTGCGATGGGAGTCATGGTGTGATAACCCTTCATCTGTTTACACTGCTCGC	2955			
TITLE Human proteases and polynucleotides encoding the same	Db	259 TGGCTCAAACACGACAGGTGTGTCATGGACACAGAGTGGAATTCCAAGATAT	318			
JOURNAL Patent: US 6881563-A 27 19-APR-2005;	Qy	2956 TGGCTCAAACACGACAGGTGTGTCATGGACACAGAGTGGAATTCCAAGATAT	3015			
FEATURES Lexicon Genetics Incorporated; The Woodlands, TX	Db	319 GGGCACTAG 327				
LOCATION/QUALIFIERS	Db	3016 GGGCACTAG 3024				
ORIGIN	Qy	76.1%; Score 249; DB 6; Length 3208;				
Best Local Similarity 100.0%;	Db	Pred. No. 2.6e-137; Mismatches 0;	Indels 0;	Gaps 0;		
Matches 249; Conservative 0;	Db	RESULT 28				
DEFINITION CO709825	Db	LOCUS CQ709825	430 bp	DNA	linear	PAT 03-FEB-2004
ACCESSION CO709825	Db	DEFINITION Sequence 54751 from Patent WO0207070737.				
VERSION CQ709825.1	Db	VERSION CQ709825.1 GI:42270679				
KEYWORD SOURCE Homo sapiens (human)	Db	ORGANISM Homo sapiens				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	Db	REFERENCE 1				
Liew,C.C., Marshall,W.E. and Zhang,H.	Db	AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.				
Compositions and methods relating to osteoarthritis	Db	TITLE Compositions and methods relating to osteoarthritis				
Patent: WO 02070737-A 14 07-12-2002;	Db	JOURNAL Patent: WO 02070737-A 14 07-12-2002;				
FEATURES	Db	LOCATION/QUALIFIERS Chondrogen Inc. (CA)				
SOURCE	Db	1. organism="Homo sapiens"				
	Db	/mol_type="unassigned DNA"				
	Db	/db_xref="taxon:9606"				
ORIGIN	Qy	63.3%; Score 207;	DB 6;	Length 430;		
Best Local Similarity 99.7%;	Db	Pred. No. 3.8e-112;	Mismatches 0;	Indels 1;	Gaps 1;	
Matches 327; Conservative 0;	Db	Query Match				
DEFINITION AX212267	Db	AX212267				
ACCESSION AX212267	Db	Sequence 27 from Patent WO0159134.	DNA	linear	PAT 06-SEP-2001	
VERSION AX212267.1	Db	3208 bp				
KEYWORD SOURCE Homo sapiens (human)	Db	AX212267				
ORGANISM Homo sapiens	Db	AX212267.1 GI:15524031				
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	Db	1. ATGGCGCGACGCGATGGATGGGATACCCGAGGGCACCAACAGGGCGGGCAAGAAG	60			
REFERENCE AUTHORS Donoho,G., Scoville,J., Turner,C.A., Friedrich,G.B., Abuin,A.,	Qy	61 CGCTTTGAGTGTAAAATGGTAATGGGATCTGGCTGGATATTGTGTGTGAT	120			
Zambrowicz,B. and Sands,A.T.	Db	21 ATGCGCGACGCGATGGATGGGATACCCGAGGGCACCAACAGGGCGGGCAAGAAG	80			
TITLE Human proteases and polynucleotides encoding the same	Db	81 CGCTTTGAGTGTAAAATGGTAATGGGATCTGGCTGGATATTGTGTGTGAT	140			
JOURNAL Patent: WO 0159134-A 27 16-AUG-2001;	Qy	121 AACTGTGCCATCTGGCTGGGTCAACACGACAGGTGTGTCAGTGGGAGTCAGTGGTGTGAT	179			
Lexicon Genetics Incorporated (US)	Db	141 AACTGTGCCATCTGGCTGGGTCAACACGACAGGTGTGTCAGTGGTGTGAT	200			
LOCATION/QUALIFIERS	Db	180 GGCCTCGCTACTTCAGAGAGGTGTCACTGTCAGTGGGAGTCAGTGGTGTGAT	239			
1. .3208	Db	201 GGCCTCGCTACTTCAGAGAGGTGTCACTGTCAGTGGGAGTCAGTGGTGTGAT	260			
/organism="Homo sapiens"	Qy	240 CTTCACAGCATCTCTGGCTGGGTCAACACGACAGGTGTGTCAGTGGGAGTCAGA	299			
/mol_type="unassigned DNA"	Db	261 CTTCACAGCATCTCTGGCTGGGTCAACACGACAGGTGTGTCAGTGGGAGTCAGA	320			
/db_xref="taxon:9606"	Qy					
ORIGIN	Qy					



		CC n=a, g, c or t Key misc	Location/Qualifiers feature Location/Qualifiers 74
Db	226 TGTGTCATTGGACAAAGAGTGGCACTAG 275		
RESULT 32			
LOCUS	AX94508	402 bp	DNA
DEFINITION	Sequence 10371 from Patent EP1033401.		
ACCESSION	AX94508		
VERSION	1	GI:40049392	
KEYWORDS	Homo sapiens (human)		
ORGANISM	Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	Dumas Milne Edwards, J.B., Duclerc, A., and Giordano, J.Y.		
AUTHORS	Expressed sequence tags and encoded human proteins		
TITLE	Patent : EP 1033401-A 10371 06-SEP-2000;		
JOURNAL	Genset (FR)		
FEATURES	source		
	1..402	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"	
ORIGIN			
Query Match	52.0%	Score 170; DB 6; Length 402;	
Best Local Similarity	100.0%	Pred. No. 6..2e-90;	
Matches	170;	Mismatches 0; Indels 0; Gaps 0;	
Qy	158 GCATAGAATGCAAGTAAACCGGCTAACGGCTTAACGGCTTACTCAGAAGTGTACTGTCGATGGG 217		
Db	106 GCATAGAATGCAAGTAAACCGGCTAACGGCTTACTCAGAAGTGTACTGTCGATGGG 165		
Qy	218 GAGTCTGTAACCATGCTTTTCACTTCCACTGGCTCGTACTCTCGGCTCAAACACGACAGG 277		
Db	166 GAGTCTGTAACCATGCTTTTCACTTCCACTGGCTCGTACTCTCGGCTCAAACACGACAGG 225		
Qy	278 TGTGTCATTGGACAAAGAGTGGCACTAG 327		
Db	226 TGTGTCATTGGACAAAGAGTGGCACTAG 275		
RESULT 33			
LOCUS	BD119236	463 bp	DNA
DEFINITION	EST and encoded human protein.		
ACCESSION	BD119236		
VERSION	GI:2331446		
KEYWORDS	JP 2002010789-A/11313.		
SOURCE	Homo sapiens (human)		
ORGANISM	Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1 (bases 1 to 463)		
AUTHORS	Edwards, J.B.D.M., Jobert, S. and Giordano, J.E.		
TITLE	EST and encoded human Protein		
JOURNAL	Patent : JP 2002010789-A 11313 15-JAN-2002;		
GENSET CORP			
COMMENT	Homo sapiens (human)		
PN	JP 2002010789-A/11313		
PD	15-JAN-2002		
PP	07-AUG-2000	JP 2002080989	
PR	05-AUG-1999	US 60/147499	
PI	JEAN BAPTIST DUMAS MILNE EDWARDS, SEVELIN JOBERT, JEAN EVE	PI	
GIORDANO			
PC	C12N15/09, C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19,	PC	
C12N1/21,			
C12N15/00, C12N15/00, C12N15/08, C12Q1/08, C12Q1/08	PC		
RESULT 34			
LOCUS	AR423683	463 bp	DNA
DEFINITION	Sequence 15180 from patent US 6639063.		
VERSION	AR423683		
KEYWORDS	GI:40178793		
SOURCE	Unknown.		
ORGANISM	Unclassified.		
REFERENCE	1 (bases 1 to 463)		
AUTHORS	Edwards, J.-B.D.M., Jobert, S. and Giordano, J.-Y.		
TITLE	EST's and encoded human Proteins		
JOURNAL	Patent : US 6639063-A 15180 28-OCT-2003;		
GENSET S.A.:			
WOX:			
FEATURES	source		
	1..463	/organism="unknown" /mol_type="genomic DNA"	
ORIGIN			
Query Match	52.0%	Score 170; DB 6; Length 463;	
Best Local Similarity	100.0%	Pred. No. 6..3e-90;	
Matches	170;	Mismatches 0; Indels 0; Gaps 0;	
Qy	158 GCATAGAATGCAAGTAAACCGGCTAACGGCTTACTCAGAAGTGTACTGTCGATGGG 217		
Db	101 GCATAGAATGCAAGTAAACCGGCTAACGGCTTACTCAGAAGTGTACTGTCGATGGG 160		
Qy	218 GAGTCTGTAACCATGCTTTCACTTCCACTGGCTCGTACTCTCGGCTCAAACACGACAGG 277		
Db	161 GAGTCTGTAACCATGCTTTCACTTCCACTGGCTCGTACTCTCGGCTCAAACACGACAGG 220		
Qy	278 TGTGTCATTGGACAAAGAGTGGCACTAG 327		
Db	221 TGTGTCATTGGACAAAGAGTGGCACTAG 270		
RESULT 35			
LOCUS	AX984377	463 bp	DNA
DEFINITION	Sequence 15180 from Patent EP1104808.		
VERSION	AX984377		
KEYWORDS	GI:40990517		

SOURCE	Homo sapiens (human)						
ORGANISM	Homo sapiens						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
	Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;						
	Hominidae; Homo.						
REFERENCE							
AUTHORS	Dumas Milne Edwards,J.B., Jobert,S. and Giordano,J.Y.						
TITLE	ESTs and encoded human proteins						
JOURNAL	Patent: EP 1104808-A 15180 06-JUN-2001;						
FEATURES	source	Location/Qualifiers					
	1. .463	/organism="Homo sapiens"					
		/mol_type="unassigned DNA"					
		/db_xref="taxon:9606"					
ORIGIN							
Query Match	52.0%	Score 170; DB 6; Length 463;					
Best Local Similarity	100.0%	Pred. No. 6.3e-90;					
Matches	170;	Conservative 0; Mismatches 0;	Indels 0;	Gaps 0;			
Qy	158	GCATAGAATGTCAGCTAACCGCGTCCGCTACTTCAGAAAGGTGATGG 217					
Db	101	GCATAGAATGTCAGCTAACCGCGTCCGCTACTTCAGAAAGGTGATGG 160					
Qy	218	GAGTCTGTAACCATGCTTTCACTTCCACTGCACTCTCGCTCTCAGACGG 277					
Db	161	GAGTCTGTAACCATGCTTTCACTTCCACTGCACTCTCGCTCTCAGACGG 220					
Qy	278	TGTGTCCATTGGACAGACAGAGTGGAATTCCAAGATGGCACTAG 327					
Db	221	TGTGTCCATTGGACAGACAGAGTGGAATTCCAAGATGGCACTAG 270					
RESULT 36							
QLOC	CQ674921	Sequence 19847 from Patent WO20070737.	370 bp	DNA	linear	PAT 03-FEB-2004	
DEFINITION							
ACCESSION	CQ674921						
VERSION	CQ674921.1						
KEYWORDS							
ORGANISM	Homo sapiens (human)						
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
	Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini;						
	Hominidae; Homo.						
REFERENCE							
AUTHORS	Liew,C.C., Marshall,W.E. and Zhang,H.						
TITLE	Compositions and methods relating to osteoarthritis						
JOURNAL	Patent: WO 02070737-A 19847 12-SEP-2002;						
FEATURES	source	Location/Qualifiers					
	1. .370	/organism="Homo sapiens"					
		/mol_type="unassigned DNA"					
		/db_xref="taxon:9606"					
ORIGIN							
Query Match	49.8%	Score 163; DB 6; Length 370;					
Best Local Similarity	9.5%	Pred. No. 9.9e-86;					
Matches	213;	Conservative 0; Mismatches 1;	Indels 0;	Gaps 0;			
Qy	114	GGTGATTACTGTGCCTCTGCAGAACCATATGATCTTGCTAGATGTCAGC 173					
Db	3	GGTGATTACTGTGCATCTGCAGAACCATATGATCTTGCTAGATGTCAGC 62					
Qy	174	TAACAGGCTCCGTTCTCAGAGGTGATCTGATGGGAGTCGTAAACCATC 233					
Db	63	TAACAGGCTCCGTTCTCAGAGGTGATCTGATGGGAGTCGTAAACCATC 122					
Qy	234	TTCACGCACTGCACTCTCGCTGGCTCAAAACACGAGCTGGTGTGCA 293					
Db	123	TTCACGCACTGCACTCTCGCTGGCTCAAAACACGAGCTGGTGTGCA 182					



ORGANISM	Homo sapiens	JOURNAL	Nat. Genet. 36 (1), 40-45 (2004)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kikkawa, E., Omura, Y., Abe, K., Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kikkawa, E., Omura, Y., Abe, K.,		
REFERENCE	Lieu, C.C., Marshall, W.E. and Zhang, H.H.	AUTHORS	Kodaishi, H., Furuya, T., Takahashi, M., Yamazaki, M., Yamazaki, S., Kaminaga, K., Katsuta, N., Sato, K., Tanikawa, M., Yamamoto, J., Irie, R., Otsuki, T., Sato, H., Wakamatstu, A., Ishii, S., Sugiyama, T., Itoh, T., Shigemoto, K., Senba, T., Matsunaga, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Nagase, T., Nomura, N., Kikuchi, H., Matsuo, Y., Yamashita, T., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
AUTHORS	Liaw, C.C., Marshall, W.E. and Zhang, H.H.	JOURNAL	Patent: WO 02070737-A 33633 12-SEP-2002; Chondrogen Inc. (CA)
FEATURES	Location/Qualifiers	source	1. 363 /org:sm="Homo sapiens" /mol type="unassigned DNA" /db_xref="taxon:9606"
ORIGIN	Query Match Score 99; DB 6; Length 363; Best Local Similarity 100.0%; Prod. No. 2. 6e-4; Matches 99; Conservative 0; Mismatches 0; Indels 0; Gaps 0; -	REFERENCE	Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kikkawa, E., Omura, Y., Abe, K., Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kikkawa, E., Omura, Y., Abe, K.,
LOCUS	AK090764	DEFINITION	AK090764 Human CDNA FLJ33445 firs, clone BRAI2000263.
ACCESSION	AK090764	VERSION	AK090764.1 GI:21748986
KEYWORDS	Oligo capping; firs (full insert sequence).	SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.	RESULT	43
REFERENCE	Ota, T., Suzuki, Y., Nishikawa, T., Otsuki, T., Sugiyama, T., Irie, R., Wakamatsu, A., Hayashi, K., Sato, H., Nagai, K., Kimura, K., Makita, H., Sekine, M., Obayashi, M., Nishi, T., Shiba, T., Tanaka, T., Ishii, S., Yamamoto, J., Saito, K., Kawai, Y., Isono, Y., Nakamura, Y., Nagahari, K., Murakami, K., Yasuda, T., Iwayanagi, T., Wagatsuma, M., Shiratori, A., Sudo, H., Hosoi, T., Kakutani, T., Koda, H., Sugawara, M., Takahashi, M., Kanda, K., Yoko, T., Furuya, T., Kikkawa, E., Omura, Y., Abe, K., Kamiyama, K., Katsuta, N., Sato, K., Tanikawa, M., Yamazaki, M., Niimori, K., Ishibashi, T., Yamashita, H., Hiraoka, S., Chiba, Y., Ishida, S., Ono, Y., Takiguchi, S., Watanabe, M., Yosida, M., Hotaru, T., Kusano, J., Kaneko, K., Takahashi, K., Hara, H., Tanase, T., Nomura, Y., Hata, H., Kondo, F., Hara, R., Takeuchi, K., Arita, M., Imose, N., Musashino, K., Yuki, H., Osima, A., Sasaki, N., Aotsuka, S., Moriya, S., Moriya, S., Momiyama, H., Ichihara, T., Shiohata, N., Sano, S., Nakagawa, S., Momiyama, H., Sato, N., Terashima, Y., Suzuki, O., Nakagawa, S., Momiyama, H., Sato, N., Shimizu, F., Wakebe, H., Hishigaki, H., Watanabe, T., Goto, Y., Sugiyama, A., Takemoto, M., Kawakami, B., Yamazaki, M., Watanabe, K., Kumagai, A., Itakura, S., Fukuzumi, Y., Fujimori, Y., Komiyama, M., Nasu, H., Taniyama, A., Fujiwara, T., Ono, T., Yamada, K., Fujii, Y., Ozaki, K., Hirao, M., Ohmori, Y., Kawabata, A., Hikiji, T., Kobatake, N., Inagaki, H., Ikeda, Y., Okamoto, S., Okitani, R., Kawakami, T., Noguchi, S., Itoh, T., Shigemoto, K., Senba, T., Matsunaga, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Oyama, M., Hata, H., Watanabe, M., Komatsu, T., Mizushima-Sugano, J., Satoh, T., Shirai, Y., Takahashi, Y., Nakagawa, K., Okumura, K., Nagase, T., Nomura, N., Kikuchi, H., Matsuo, Y., Yamashita, T., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.		
TITLE	Complete sequencing and characterization of 21,243 full-length human cDNAs	JOURNAL	Nat. Genet. 36 (1), 40-45 (2004)
PUBMED	14702039	AUTHORS	Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kikkawa, E., Omura, Y., Abe, K., Ninomiya, K., Wagatsuma, M., Kanda, K., Kondo, H., Yokoi, T., Kikkawa, E., Omura, Y., Abe, K.,
ARTICLE	2	JOURNAL	Kodaishi, H., Furuya, T., Takahashi, M., Yamazaki, M., Yamamoto, J., Irie, R., Otsuki, T., Sato, H., Wakamatstu, A., Ishii, S., Sugiyama, T., Itoh, T., Shigemoto, K., Senba, T., Matsunaga, K., Nakajima, Y., Mizuno, T., Morinaga, M., Sasaki, M., Togashi, T., Nagase, T., Nomura, N., Kikuchi, H., Matsuo, Y., Yamashita, T., Nakai, K., Yada, T., Nakamura, Y., Ohara, O., Isogai, T. and Sugano, S.
COMMENT	2	COMMENT	NEDO Human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5' & 3' end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; Clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
FEATURES	1	FEATURES	1. 1871 /organism="Homo sapiens" /mol type="mRNA" /db_xref="Taxon:9606" /clone="BRAI200263" /tissue type="alzheimer cortex" /clone Lib="BRAI22" /note="Cloning vector: pME18SFL3"
ORIGIN	1	ORIGIN	Qy 229 CATGGTTTCACTTCACCTCCACTGCACTCTCGATCTCTGGTCAAACACAGGTGTCATTG 288 Db 1599 CATGGTTTCACTTCACCTCCACTGCACTCTCGCTGGTCAAACACAGACGGTGTCCATTG 1658 Qy 289 GACAACAGAGTGGAATCCAAAGATGGGACTAG 327 Db 1659 GACAACAGAGTGGAATCCAAAGATGGGACTAG 1697
FEATURES	1	FEATURES	Query Match Score 99; DB 8; Length 1871; Best Local Similarity 100.0%; Prod. No. 2. 8e-47; Mismatches 0; Indels 0; Gaps 0;
source	1	source	Qy 229 CATGGTTTCACTTCACCTCCACTGCACTCTCGATCTCTGGTCAAACACAGGTGTCATTG 288 Db 1599 CATGGTTTCACTTCACCTCCACTGCACTCTCGCTGGTCAAACACAGACGGTGTCCATTG 1658 Qy 289 GACAACAGAGTGGAATCCAAAGATGGGACTAG 327 Db 1659 GACAACAGAGTGGAATCCAAAGATGGGACTAG 1697
LOCATION	1	LOCATION	Search completed: March 15, 2006, 18:00:43 Job time : 2416 secs

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**Nucleic = nucleic search using SW model**

run on: March 8, 2006 15:18:35 ; Search time 659.377 Seconds  
 run on: March 8, 2006 15:18:35 ; Search time 659.377 Seconds  
 by nuclear - nuclear search, using bw model  
 Sequence 52747/  
 Sequence 52747/  
 Sequence 50604/  
 Sequence 50604/

	Sequence 27, App without arguments /	Sequence 27, App with arguments /
4100.974 Million cell updates/sec	3.2	3.3

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scoring table: IDENTITY_NUC
Gapo 10.0 , Gapext 1.0

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searched: 9793542 seqs, 4134689005 residues

total number of hits satisfying chosen parameters:	19587084	minimum DB seq length:	8	Sequence 46883, Sequence 46883,
		44	208.8	63.9
		45	208.8	63.9
				US-10-242-535A-46883 US-10-085-783A-46883

## ALIGNMENTS

Maximum Match 100%  
Listing first 45 summaries  
**RESULT 1**

Published Applications NA Main: \*  
1: /cgn2\_6/picodata/1/pubdata/US07\_PUBCOMB.seq: \*  
Database : US-10-242-53A-435 //  
; Sequence 43377, Application US/10242535A  
; Publication No. US20040013663A1

GENERAL INFORMATION:  
APPLICANT: Chondrodene Inc.  
APPLICANT: Liew, C.C.

FILE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
CURENT APPLICATION NUMBER: US/10/2422-535A  
FILE NUMBER: 4221/2005

8: /cgn2\_6/picdata/1/pubnna/US10D\_PUBCOMB.seq;\*  
9: /cgn2\_6/picdata/1/pubnna/US10E\_PUBCOMB.seq;\*  
10: /cam5\_6/prodara/1/mibmona/US11\_PUBCOMR.seq;\*

; CURRENT FILING DATE: 2002-09-12  
; PRIORITY APPLICATION: US 10/095,783  
; PRIORITY FILING DATE: 2002-02-28

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being examined.

and is derived by analysis of the total score distribution.

CROSS-REFERENCE TO RELATED APPLICATIONS

PRIOR FILING DATE: 2001-03-12  
PRIOR APPLICATION NUMBER: US 60/271,955

二

1 SOFTWARE: PatentIn version 3.2  
1 SEQ ID NO: 43377  
1 LENGTH: 433

1	327	100.0	433	7	US-10-242-533A-43377	Sequence 43377, A
2	327	100.0	433	7	US-10-242-533A-43377	Sequence 43377, A
3	327	100.0	453	7	US-10-242-555A-36205	Sequence 25505
						TYPE: DNA ; ORGANISM: Human

	Matches	Coverage	Conservative	Mismatches	Indels	Gaps
7	327	100.0	471	7	US-10-242-553A-57254	Sequence 57254, A
8	327	100.0	471	7	US-10-085-783A-57254	Sequence 57254, A
9	327	100.0	471	7	US-10-242-553A-57254	Sequence 57254, A
10	327	100.0	471	7	US-10-242-553A-57254	Sequence 57254, A

1	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Db	20
2	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 5,068, A	Sequence 5,068, A	20
3	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
4	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
5	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
6	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
7	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
8	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
9	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
10	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
11	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
12	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
13	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
14	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
15	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
16	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
17	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
18	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
19	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20
20	AAGGCGGGCCACCAACAGGGCGGGAGAAG	Sequence 3, Appli	Sequence 3, Appli	20

12	322	100.0	523	7	US-10-222-1022	Sequence 46222, A	Qy	61
13	327	100.0	523	7	US-10-222-7-783A-46222	Sequence 46222, A		
14	325	99.4	476	3	US-09-918-995-17191	Sequence 17191, A		

C	321.8	98.4	454.3	7	US-10-138-8633-11311	Sequence 1
C	316	96.6	430	7	US-10-242-5633-50751	Sequence 2
C	316	96.6	430	7	US-10-085-7633A-54751	Sequence 3
C	316	96.6	430	7	US-10-085-7633A-54751	Sequence 4
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C	18	308.8	94.4	4476	8	US-10-57-930-25664	Sequence 25604, A	Db
C	19	302.4	92.5	3847	3	US-09-960-352-4677	Sequence 4677, Ap	
C	20	301.2	92.1	5347	6	US-10-20-965-99	Sequence 99, Ap	
C	21	301.2	92.1	5347	6	US-10-20-965-99	Sequence 99, Ap	
								140 AACTGTGCATCTGAGGAACCACTATTGGATCTTTGCATAGAATGTCAGCTAACAG 1

QY 241 TTCCAACTGGATCTCTGCTGGCTCAAACAGAACAGGTGTCATTGGCACAACAGAGAG 300  
 Db 260 TTCCAACTGGATCTCTGCTGGCTCAAACAGAACAGGTGTCATTGGCACAACAGAGAG 319

QY 301 TGGGAATTCAAAAGTATGGCACTAG 327  
 Db 320 TGGGAATTCAAAAGTATGGCACTAG 346

RESULT 2  
 US-10-085-783A-43377  
 ; Sequence 43377, Application US/10085783A  
 ; Publication No. US20040037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; INVENTOR: Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US/10/085,783A  
 ; CURRENT FILING DATE: 2002-02-08  
 ; PRIORITY APPLICATION NUMBER: US 60/305,340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIORITY APPLICATION NUMBER: US 60/275,017  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIORITY APPLICATION NUMBER: US 60/271,955  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIORITY APPLICATION NUMBER: US 60/271,955  
 ; PRIORITY FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 5894  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO: 35025  
 ; LENGTH: 453  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-242-535A-35025

Query Match Score 100.0%; Score 327; DB 7; Length 453;  
 Best Local Similarity 100.0%; Pred. No. 5.e-104;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCAGGGATGGATGGATGGATACCCGAGGGCACCACACCGGGAGAG 60  
 Db 24 ATGGGGAGGGATGGATGGATACCCGAGGGCACCACACCGGGAGAG 83

QY 61 CGCTTTGAGTGAAAAGTGGAACTAGGCTCTAGGCCAGTGGCTCTGGGATATTGGCTTGAT 120  
 Db 84 CGCTTTGAGTGAAAAGTGGAACTAGGCTCTAGGCCAGTGGCTCTGGGATATTGGCTTGAT 143

QY 121 AACCTGGCATCTGGGACCAATTGGATGTTGGATAGATGTAAGCTAACAG 180  
 Db 144 AACCTGGCATCTGGGACCAATTGGATGTTGGATAGATGTAAGCTAACAG 203

QY 181 GCCTCCGGTACTCTAGAAGGTGACTGTGCATGGGAGTCCTTAACCATGGTTTCAC 240  
 Db 204 GCCTCCGGTACTCTAGAAGGTGACTGTGCATGGGAGTCCTTAACCATGGTTTCAC 263

QY 1 ATGGCGCAGGGATGGATGGATACCCGAGGGCACCACACCGGGAGAG 60  
 Db 20 ATGGCGCAGGGATGGATGGATACCCGAGGGCACCACACCGGGAGAG 79

QY 61 CGCTTTGAGTGAAAAGTGGAACTAGGCTCTGGGATATTGGCTTGAT 120  
 Db 80 CGCTTTGAGTGAAAAGTGGAACTAGGCTCTGGGATATTGGCTTGAT 139

QY 121 AACCTGGCATCTGGGACCAATTGGATGTTGGATAGATGTAAGCTAACAG 180  
 Db 140 AACCTGGCATCTGGGACCAATTGGATGTTGGATAGATGTAAGCTAACAG 199

QY 181 GCCTCCGGTACTCTAGAAGGTGACTGTCCATGGGAGTCCTGTAACCATGGTTTCAC 240  
 Db 200 GCCTCCGGTACTCTAGAAGGTGACTGTCCATGGGAGTCCTGTAACCATGGTTTCAC 259

QY 241 TTCCAACTGGCATCTGGCTCAAACAGAACAGGTGTCATTGGCACAACAGAGAG 300  
 Db 260 TTCCAACTGGCATCTGGCTCAAACAGAACAGGTGTCATTGGCACAACAGAGAG 319

QY 301 TGGGAATTCAAAAGTATGGCACTAG 327  
 Db 320 TGGGAATTCAAAAGTATGGCACTAG 346

RESULT 3  
 US-10-242-535A-35025  
 ; Sequence 35025, Application US/10242535A  
 ; Publication No. US200400313663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; INVENTOR: Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2005

Query Match Score 100.0%; Score 327; DB 7; Length 453;  
 Best Local Similarity 100.0%; Pred. No. 5.e-104;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCAGGGATGGATGGATACCCGAGGGCACCACACCGGGAGAG 60  
 Db 24 ATGGGGAGGGATGGATGGATACCCGAGGGCACCACACCGGGAGAG 83

QY 61 CGCTTTGAGTGAAAAGTGGAACTAGGCTCTAGGCCAGTGGCTCTGGGATATTGGCTTGAT 120  
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QY 121 AACCTGGCATCTGGGACCAATTGGATGTTGGATAGATGTAAGCTAACAG 180  
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 Db 204 GCCTCCGGTACTCTAGAAGGTGACTGTGCATGGGAGTCCTTAACCATGGTTTCAC 263

QY 1 ATGGCGCAGGGATGGATGGATACCCGAGGGCACCACACCGGGAGAG 60  
 Db 20 ATGGCGCAGGGATGGATGGATACCCGAGGGCACCACACCGGGAGAG 79

QY 61 CGCTTTGAGTGAAAAGTGGAACTAGGCTCTGGGATATTGGCTTGAT 120  
 Db 80 CGCTTTGAGTGAAAAGTGGAACTAGGCTCTGGGATATTGGCTTGAT 139

QY 121 AACCTGGCATCTGGGACCAATTGGATGTTGGATAGATGTAAGCTAACAG 180  
 Db 140 AACCTGGCATCTGGGACCAATTGGATGTTGGATAGATGTAAGCTAACAG 199

QY 181 GCCTCCGGTACTCTAGAAGGTGACTGTCCATGGGAGTCCTGTAACCATGGTTTCAC 240  
 Db 200 GCCTCCGGTACTCTAGAAGGTGACTGTCCATGGGAGTCCTGTAACCATGGTTTCAC 259

QY 241 TTCCAACTGGCATCTGGCTCAAACAGAACAGGTGTCATTGGCACAACAGAGAG 300  
 Db 260 TTCCAACTGGCATCTGGCTCAAACAGAACAGGTGTCATTGGCACAACAGAGAG 319

QY 301 TGGGAATTCAAAAGTATGGCACTAG 327  
 Db 320 TGGGAATTCAAAAGTATGGCACTAG 346

RESULT 4  
 US-10-085-783A-35025  
 ; Sequence 35025, Application US/10085783A  
 ; Publication No. US20040037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Liew, C.C.  
 ; INVENTOR: ChondroGene Inc.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US/10/085,783A  
 ; CURRENT FILING DATE: 2002-02-28  
 ; PRIORITY APPLICATION NUMBER: US 60/305,340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIORITY APPLICATION NUMBER: US 60/275,017  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIORITY APPLICATION NUMBER: US 60/271,955  
 ; PRIORITY FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 5894  
 ; SEQ ID NO: 35025  
 ; LENGTH: 453  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-10-085-783A-35025

Query Match Score 100.0%; Score 327; DB 7; Length 453;

Best Local Similarity 100.0%; Pred. No. 5.5e-104; Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 200 GCGTCGGCTACTTCAGAAGAGTGTACTGTGCATGGGAGCTGTAAACCATGGTTTCAC 259  
 Qy 241 TTCCACTGCGATCTCCTGCTGCTCAAACAGCAAGCTGTTCACTGGACAAAGAGAG 300  
 Db 260 TTCCACTGCGATCTCCTGCTGCTCAAACAGCAAGCTGTTCACTGGACAAAGAGAG 319

Db 61 CGCTTGAAGTAAAAGTGGAAATGCGTGTGGCTCTGGCTGGGATATGTGGTTGAT 120  
 Qy 301 TGGGAATTCCAAGAAGTGGCACTGGCTGCTGGGATATGTGGTTGAT 327  
 Db 320 TGGGAATTCCAAGAAGTGGCACTGGCTGCTGGGATATGTGGTTGAT 346

RESULT 6  
 US-10-085-783A-39933  
 ; Sequence 39933, Application US/10085783A  
 ; Publication No. US2004037841A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2002  
 ; CURRENT APPLICATION NUMBER: US/10/085,783A  
 ; CURRENT FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/305,340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIORITY NUMBER: US 60/275,017  
 ; PRIORITY FILING DATE: 2001-03-12  
 ; PRIORITY APPLICATION NUMBER: US 60/271,955  
 ; PRIORITY FILING DATE: 2001-02-28  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 39933  
 ; LENGTH: 467  
 ; ORGANISM: Human  
 US-10-085-783A-39933

Query Match 100.0%; Score 327; DB 7; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-104; Mismatches 0; Indels 0; Gaps 0;

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 Db 20 ATGGGGCAGCGATGGATGGATGCCAGCCACACAGGGCGGGCAAGAGAG 79  
 Qy 61 CGCTTGAAGTAAAAGTGGAAATGCGTGTGGATATGTGGTTGAT 120  
 Db 80 CGCTTGAAGTAAAAGTGGAAATGCGTGTGGATATGTGGTTGAT 139  
 Qy 121 AACCTGGCCATCTGGGACCAATTGGATCTGGCATAGAATGTCAGCTAACCAAG 180  
 Db 140 AACCTGGCCATCTGGGACCAATTGGATCTGGCATAGAATGTCAGCTAACCAAG 199  
 Qy 161 CGCTTGAAGTAAAAGTGGAAATGCGTGTGGATATGTGGTTGAT 120  
 Db 180 CGCTTGAAGTAAAAGTGGAAATGCGTGTGGATATGTGGTTGAT 139

RESULT 7  
 US-10-242-535A-57254  
 ; Sequence 57254, Application US/10242535A  
 ; Publication No. US2004011663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

US-10-242-535A-39933  
 ; Sequence 39933, Application US/10242535A  
 ; Publication No. US2004011663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 ; FILE REFERENCE: 4231/2005  
 ; CURRENT APPLICATION NUMBER: US/10/242,535A  
 ; CURRENT FILING DATE: 2002-09-12  
 ; PRIOR APPLICATION NUMBER: US 10/085,783  
 ; PRIOR FILING DATE: 2002-02-28  
 ; PRIOR APPLICATION NUMBER: US 60/305,340  
 ; PRIOR FILING DATE: 2001-07-13  
 ; PRIOR APPLICATION NUMBER: US 60/275,017  
 ; PRIOR FILING DATE: 2001-03-12  
 ; PRIOR APPLICATION NUMBER: US 60/271,955  
 ; NUMBER OF SEQ ID NOS: 58994  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 39933  
 ; LENGTH: 467  
 ; ORGANISM: Human  
 US-10-242-535A-39933

Query Match 100.0%; Score 327; DB 7; Length 467;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-104; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCCGAGGGATGGATGGATGCCAGGGCAACACAGGGCGGGCAAGAGAG 60  
 Db 20 ATGGCCGAGGGATGGATGCCAGGGCAACACAGGGCGGGCAAGAGAG 79  
 Qy 241 TTCCACTGCGATCTCCTGCTGCTCAAACAGCAAGCTGTTCACTGGTTTCAC 259  
 Db 260 TTCCACTGCGATCTCCTGCTGCTCAAACAGCAAGCTGTTCACTGGTTTCAC 319  
 Qy 301 TGGGAATTCCAAGAAGTGGCACTGGCTGCTGGGATATGTGGTTGAT 327  
 Db 320 TGGGAATTCCAAGAAGTGGCACTGGCTGCTGGGATATGTGGTTGAT 346

RESULT 7  
 US-10-242-535A-57254  
 ; Sequence 57254, Application US/10242535A  
 ; Publication No. US2004011663A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: ChondroGene Inc.  
 ; Liew, C.C.  
 ; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis

FILE REFERENCE: 4231/2005  
 CURRENT APPLICATION NUMBER: US/10/242,535A  
 PRIOR FILING DATE: 2002-09-12  
 PRIOR APPLICATION NUMBER: US 10/085,783  
 PRIOR FILING DATE: 2002-02-28  
 PRIOR APPLICATION NUMBER: US 60/305,340  
 PRIOR FILING DATE: 2001-07-13  
 PRIOR APPLICATION NUMBER: US 60/275,017  
 PRIOR FILING DATE: 2001-03-12  
 PRIOR APPLICATION NUMBER: US 60/271,955  
 PRIOR FILING DATE: 2001-02-28  
 NUMBER OF SEQ ID NOS: 58934  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 57254  
 LENGTH: 471  
 TYPE: DNA  
 ORGANISM: Human  
 US-10-242-535A-57254

Query Match 100.0%; Score 327; DB 7; Length 471;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-104;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCCGGAGCGATGGATGCGATACCCGAGGGCAACACGGGGCAAGAG 60  
 Db 17 ATGCCGGAGCGATGGATGCGATGGATACCCGAGGGCAACACGGGGCAAGAG 76

Qy 61 CGCTTGAACTGAAGTGAAGATGGCATGGATTGGCTGGGATTTGTTGAT 120  
 Db 77 CGCTTGAACTGAAGTGAAGATGGCATGGATTGGCTGGGATTTGTTGAT 136

Query Match 100.0%; Score 327; DB 7; Length 471;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-104;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCAGGGATGTGGATAACCCGAGGGCACCAACACGGGGAAAGAG 60  
 Db 17 ATGGCGCAGGGATGTGGATAACCCGAGGGCACCAACACGGGGAAAGAG 76

Qy 61 CGCTTGAACTGAAGTGAAGATGGCATGGCTGGGATTTGTTGAT 120  
 Db 77 CGCTTGAACTGAAGTGAAGATGGCATGGCTGGGATTTGTTGAT 136

RESULT 9  
 US-10-242-535A-5635A  
 Sequence 5635A, Application US/10242535A  
 / Publication No. US20040012663A1  
 / GENERAL INFORMATION:  
 / APPLICANT: ChondroGene Inc.  
 / INVENTION: Compositions and Methods Relating to Osteoarthritis  
 / FILE REFERENCE: 4231/2005  
 / CURRENT APPLICATION NUMBER: US/10/242,535A  
 / CURRENT FILING DATE: 2002-09-12  
 / PRIOR APPLICATION NUMBER: US 10/085,783  
 / PRIOR FILING DATE: 2002-02-28  
 / PRIOR APPLICATION NUMBER: US 60/305,340  
 / PRIOR FILING DATE: 2001-07-13  
 / PRIOR APPLICATION NUMBER: US 60/275,017  
 / PRIOR FILING DATE: 2001-03-12  
 / PRIOR APPLICATION NUMBER: US 60/271,955  
 / NUMBER OF SEQ ID NOS: 58934  
 / SOFTWARE: PatentIn version 3.2  
 / SEQ ID NO: 5635A  
 / LENGTH: 472  
 / TYPE: DNA  
 / ORGANISM: Human  
 / FEATURE:  
 / NAME/KEY: misc feature  
 / LOCATION: (437)..(437)  
 / OTHER INFORMATION: n is a, c, g, or t  
 / FEATURE:  
 / NAME/KEY: misc feature  
 / LOCATION: (455)..(455)  
 / OTHER INFORMATION: n is a, c, g, or t

US-10-085-783A-57254  
 Sequence 57254, Application US/10085783A  
 / GENERAL INFORMATION:  
 / APPLICANT: ChondroGene Inc.  
 / INVENTION: Compositions and Methods Relating to Osteoarthritis  
 / FILE REFERENCE: 4231/2002  
 / CURRENT APPLICATION NUMBER: US/10/085,783A  
 / CURRENT FILING DATE: 2002-02-28  
 / PRIOR APPLICATION NUMBER: US 60/305,340  
 / PRIOR FILING DATE: 2001-07-13  
 / PRIOR APPLICATION NUMBER: US 60/275,017  
 / PRIOR FILING DATE: 2001-03-12  
 / PRIOR APPLICATION NUMBER: US 60/271,955  
 / NUMBER OF SEQ ID NOS: 58934  
 / SOFTWARE: PatentIn version 3.2  
 / SEQ ID NO: 57254  
 / LENGTH: 471  
 / TYPE: DNA  
 / ORGANISM: Human  
 / US-10-085-783A-57254

Query Match 100.0%; Score 327; DB 7; Length 472;  
 Best Local Similarity 100.0%; Pred. No. 5.6e-104;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCAGGGATGGATGCGATACCCGAGGGCACCAACAGGGCGGGCAAGAG 60  
 Db 20 ATGGCGCAGGGATGGATGCGATACCCGAGGGCACCAACAGGGCGGGCAAGAG 79

Qy 61 CGCTTGAACTGAAGTGAAGATGGCATGGCTGGGATTTGTTGAT 120



Publication No. US20040013663A1  
 GENERAL INFORMATION:  
 APPLICANT: ChondroGene Inc.  
 INVENTOR: Liew, C. C.  
 TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
 FILE REFERENCE: 4231/2005  
 CURRENT APPLICATION NUMBER: US/10/242,515A  
 CURRENT FILING DATE: 2002-09-12  
 PRIOR APPLICATION NUMBER: US 10/085,783  
 PRIOR FILING DATE: 2002-02-28  
 PRIOR APPLICATION NUMBER: US 60/305,340  
 PRIOR FILING DATE: 2001-07-13  
 PRIOR APPLICATION NUMBER: US 60/275,017  
 PRIOR FILING DATE: 2001-03-12  
 PRIOR APPLICATION NUMBER: US 60/271,955  
 PRIOR FILING DATE: 2001-02-28  
 NUMBER OF SEQ ID NOS: 58994  
 SOFTWARE: PatentIn version 3.2  
 SEQ ID NO: 46292  
 LENGTH: 523  
 TYPE: DNA  
 ORGANISM: Human  
 US-10-242-515A-46292

---

Query Match 100.0%; Score 327; DB 7; Length 523;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-104;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCGCAGGATGGTGGATACCCGAGGGCAACAGCGGGGGAAAGAG 60  
 Db 19 ATGGCGCAGGATGGTGGATACCCGAGGGCAACAGCGGGGGAAAGAG 78

QY 61 CGCTTGAAAGTGAAGAAAGTGGAACTTATGGATCATAGATGGTGGTAT 120  
 Db 79 CGCTTGAAAGTGAAGAAAGTGGAACTTATGGATCATAGATGGTGGTAT 138

QY 121 AACTGTGCCATCTGGAGGACCATTTGGATGGTGGCTGGGCTGGGATGGTGGTAT 180  
 Db 139 AACTGTGCCATCTGGAGGACCATTTGGATGGTGGCTGGGCTGGGATGGTGGTAT 198

QY 181 GCGTCGGCTACTTCAGAAGAGTGTACTCTGGCATGGGAGCTCTTAACCCATGGTGGCTGGGCTGGGATGGTGGTAT 240  
 Db 199 GCGTCGGCTACTTCAGAAGAGTGTACTCTGGCATGGGAGCTCTTAACCCATGGTGGCTGGGCTGGGATGGTGGTAT 258

QY 241 TTCCACTGCACTCTTCGCTGGCTAAACACGACAGGTGGTGGCTGGGATGGTGGTAT 300  
 Db 259 TTCCACTGCACTCTTCGCTGGCTAAACACGACAGGTGGTGGCTGGGATGGTGGTAT 318

RESULT 14  
 US-09-918-995-17191  
 Sequence 17191, Application US/09918995  
 Publication No. US20030073623A1  
 GENERAL INFORMATION:  
 APPLICANT: Hyseq, Inc.  
 TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED  
 FROM VARIOUS CDNA LIBRARIES  
 FILE REFERENCE: 20411-756  
 CURRENT APPLICATION NUMBER: US/09/918,995  
 CURRENT FILING DATE: 2001-07-30  
 PRIOR APPLICATION NUMBER: US/09/235,076  
 PRIOR FILING DATE: 1999-01-20  
 NUMBER OF SEQ ID NOS: 38054  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 17191  
 LENGTH: 476  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: misc\_feature  
 LOCATION: (1)..(476)  
 OTHER INFORMATION: n = A,T,C or G  
 US-09-918-995-17191

---

Query Match 99.4%; Score 325; DB 3; Length 476;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-103;  
 Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GGGCGAGGATGGATGGTGGATACCCGAGGGACCAACAGCGGGCTGGGCAAGAAGGC 62  
 Db 74 GGGCGAGGATGGATGGTGGATACCCGAGGGACCAACAGCGGGCTGGGCAAGAAGGC 133

QY 63 CTTGAAGTGAAGAAAGTGGATGGTGGCTGGGCTGGGATATGGTGGTGGTATAA 122  
 Db 134 CTTGAAGTGAAGAAAGTGGATGGTGGCTGGGCTGGGATATGGTGGTGGTATAA 193

QY 123 CTGTCGCATCTGCGAGAACCATATGGATCTTGGATAGAATGTCAGCTAACCGGC 182  
 SEQ ID NO 46292

Db 194 CTGTGCCATCTGAGAACACATTATTGGATCTTGATAGAATGTCAGCTAACAGGC 253  
 Qy 183 GTCCGTACTCAGAAAGTGTACTCGCATGGAGTGTACATGTTCACT 242  
 Db 254 GTCCGTACTCAGAAAGTGTACTCGCATGGAGTGTACATGTTCACT 313  
 Qy 243 CCACTGCATCTCGTGGCTCAAACACGACAGGTGTACTCGCATGGAGTGTACATGTTCACT 302  
 Db 314 CCACTGCATCTCGTGGCTCAAACACGACAGGTGTACATGACAACAGAGTG 373  
 Qy 303 GGAATTCCAAAGTAGTGGCACTAG 327  
 Db 374 GGAATTCCAAAGTAGTGGCACTAG 398

RESULT 15  
 US-10-198-846-11311/c  
 Sequence 11311, Application US/10198846  
 Publication No. US20030099974A1  
 GENERAL INFORMATION:  
 APPLICANT: Lillie, James  
 APPLICANT: Xu, Yongxiao  
 APPLICANT: Wang, Youhen  
 APPLICANT: Steinmann, Kathleen  
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 TREATMENT OF BREAST CANCER  
 FILE REFERENCE: MRI-049  
 CURRENT APPLICATION NUMBER: US/10/198,846  
 CURRENT FILING DATE: 2002-07-18  
 PRIOR APPLICATION NUMBER: 60/306,220  
 PRIOR FILING DATE: 2001-07-18  
 NUMBER OF SEQ ID NOS: 14084  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 11311  
 LENGTH: 4543  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-198-846-11311

Query Match 98.4%; Score 321.8; DB 5; Length 4543;  
 Best Local Similarity 99.4%; Pred. No. 1e-10;  
 Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 APPLICANT: Steinmann, Kathleen  
 APPLICANT: Xu, Yongxiao  
 APPLICANT: Wang, Youhen  
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 TREATMENT OF BREAST CANCER  
 FILE REFERENCE: MRI-049  
 CURRENT APPLICATION NUMBER: US/10/198,846  
 CURRENT FILING DATE: 2002-07-18  
 PRIOR APPLICATION NUMBER: 60/306,220  
 PRIOR FILING DATE: 2001-07-18  
 NUMBER OF SEQ ID NOS: 14084  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 11311  
 LENGTH: 4543  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-198-846-11311  
 Query Match 98.4%; Score 321.8; DB 5; Length 4543;  
 Best Local Similarity 99.4%; Pred. No. 1e-10;  
 Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 APPLICANT: Steinmann, Kathleen  
 APPLICANT: Xu, Yongxiao  
 APPLICANT: Wang, Youhen  
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 TREATMENT OF BREAST CANCER  
 FILE REFERENCE: MRI-049  
 CURRENT APPLICATION NUMBER: US/10/198,846  
 CURRENT FILING DATE: 2002-07-18  
 PRIOR APPLICATION NUMBER: 60/306,220  
 PRIOR FILING DATE: 2001-07-18  
 NUMBER OF SEQ ID NOS: 14084  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 11311  
 LENGTH: 4543  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-198-846-11311  
 Query Match 98.4%; Score 321.8; DB 5; Length 4543;  
 Best Local Similarity 99.4%; Pred. No. 1e-10;  
 Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 APPLICANT: Steinmann, Kathleen  
 APPLICANT: Xu, Yongxiao  
 APPLICANT: Wang, Youhen  
 TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS  
 FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND  
 TREATMENT OF BREAST CANCER  
 FILE REFERENCE: MRI-049  
 CURRENT APPLICATION NUMBER: US/10/198,846  
 CURRENT FILING DATE: 2002-07-18  
 PRIOR APPLICATION NUMBER: 60/306,220  
 PRIOR FILING DATE: 2001-07-18  
 NUMBER OF SEQ ID NOS: 14084  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 11311  
 LENGTH: 4543  
 TYPE: DNA  
 ORGANISM: Homo sapiens  
 US-10-198-846-11311  
 Query Match 98.4%; Score 321.8; DB 5; Length 4543;  
 Best Local Similarity 99.4%; Pred. No. 1e-10;  
 Matches 323; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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RESULT 2  
 US-11-096-568A-26820  
 ; Sequence 26820, Application US/11096568A  
 ; Publication No. US20060048240A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexandrov, Nickolai et al.  
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
 ; TITLE OF INVENTION: Therby  
 ; FILE REFERENCE: 2750-1592PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/096, 568A  
 ; NUMBER OF SEQ ID NOS: 34471  
 ; SEQ ID NO: 26820  
 ; LENGTH: 693  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays subsp. mays  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(693)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 13622871  
 US-11-096-568A-26820

Query Match 52.7%; Score 172.4; DB 9; Length 348;  
 Best Local Similarity 77.4%; Pred. No. 8.6e-45;  
 Matches 209; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

Qy 57 GAGGGCTTTGAGGTAAAAAGTGGAATGCACTGAGCTTGGGATATGGCT 116  
 Db 78 GAAAGATTGAAATTAAGAATGGATCTGGGATATGGCT 137

Qy 117 TGATAACTGTGCCATTGAGAACATTAGATGATTTGGCTAGATGCTAAGCTAA 176  
 Db 138 TGATAACTGTGCCATTGAGAACATTAGATGATTTGGCTAGATGCTAAGCTAA 197

Qy 177 CCAGCGTCGCTACTCAGAACAGTGACTCTGCAACCTGCTTCAACCGCTT 236  
 Db 198 TCAAGCTAGTGGCACTAGTGAAATGCACTGCTGGGGCTTCAACCGCTT 257

Qy 237 TCACTTCCACTGCACTCTCGCTGGCTAAAAGAGAACGGTGTCCATTGGACAAACG 296  
 Db 258 TCACTTCCACTGCACTCAGAGATGGCTCAAACCTGTCAAAGTGTCCTG 317

Qy 297 AGAGTGGAAATTCCAAGATGGCAGTAACTGCTGACTA 326  
 Db 318 CGACTGGAAATTCCAGAAATATGGCTACTA 347

RESULT 4  
 US-11-096-568A-14405  
 ; Sequence 14405, Application US/11096568A  
 ; Publication No. US20060048240A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexandrov, Nickolai et al.  
 ; TITLE OF INVENTION: Therby  
 ; FILE REFERENCE: 2750-1594PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/096, 568A  
 ; CURRENT FILING DATE: 2005-04-01  
 ; NUMBER OF SEQ ID NOS: 34471  
 ; SEQ ID NO: 14405  
 ; LENGTH: 432  
 ; TYPE: DNA  
 ; ORGANISM: Zea mays subsp. mays  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(432)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 4776740  
 US-11-096-568A-14405

Query Match 51.9%; Score 169.8; DB 9; Length 432;  
 Best Local Similarity 77.0%; Pred. No. 6.2e-44;  
 Matches 207; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

Qy 58 AAGGGCTTCAAGTGAAGTGGAAATGCACTGAGCTGGCTGGGATATTGGCT 117  
 Db 171 AAGGCTTCGAGATAAGAGTGGAAACGGCTGGCTCTGGCTGGCATGTGCT 230

Qy 118 GATAACTGSGCCATCTGCAGGAACCACATTATGGATCTTGCATAAGATGCAAGCTAAC 177  
 Db 231 GACAATGCSCCATCTGCCCAACCACATGGACCTTGCATGCCAGGGAAC 290

Qy 178 CAGGGCTCGTACTCAGAGATGCTGAGTGGAGTGTGACCATGCTT 237  
 Db 291 CAGGGAGGCGGCCACAGGGAGTCACGGTGGCAATTGGCAACCATGCAATTC 350

Qy 238 CACTTCCACTGCACTCTCGCTGGCTCAAACACGACAACTGGTCATGGCAACAGA 297  
 Db 351 CACTTCACTGCACTGCAAGACCGCTCAAGTGCCCTTGACACATG 410

Qy 298 GAGTGGAAATCCAAAGATGGGACTAG 327  
 Db 411 GAGTGGAGTCCAGAGATGGTCACTAG 440

RESULT 3  
 US-11-096-568A-28569  
 ; Sequence 28569, Application US/11096568A  
 ; Publication No. US20060048240A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Alexandrov, Nickolai et al.  
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides  
 ; TITLE OF INVENTION: Therby  
 ; FILE REFERENCE: 2750-1592PUS2  
 ; CURRENT APPLICATION NUMBER: US/11/096, 568A  
 ; CURRENT FILING DATE: 2005-04-01  
 ; NUMBER OF SEQ ID NOS: 34471  
 ; SEQ ID NO: 28569  
 ; LENGTH: 348  
 ; TYPE: DNA  
 ; ORGANISM: Arabidopsis thaliana  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1)..(348)  
 ; OTHER INFORMATION: Ceres Seq. ID no. 3017472  
 US-11-096-568A-28569

Qy 58 CACTTCACTGCACTCTCGCTGGCTCAAACACGAGTGGCTGACATGGCT 297  
 Db 178 CAGGGCTCCGCTACTTCAGAGATGGTCACTGGCTGAACTATGGCTAAT 237  
 Db 281 CAGGCCAGCGCTACAGTGGAAATGCACTGGCTTCAACGTT 340

Qy 238 CACTTCACTGCACTCTCGCTGGCTCAAACACGAGTGGCTGACATGGCT 400  
 Db 341 CACTTCACTGCACTGCAAGATGGTAAAGACTCTGCAATGGCT 400

Qy 298 GAGTGGAAATCCAAAGATGGGACTA 326  
 Db 401 GAGTGGAGTCCAGAAATATGGTCACTA 429

US-10-932-182A-2279  
*i* Sequence 2279, Application US/10932182A  
*i* Publication No. US200604625A1  
*i* GENERAL INFORMATION:  
*i* APPLICANT: NAKAO, YOSHIHIRO  
*i* APPLICANT: NAKAMURA, NORIHIRO SA  
*i* APPLICANT: KODAMA, YUKIKO  
*i* APPLICANT: FUJIMURA, TOMOKO  
*i* APPLICANT: ASHIKARI, TOSHIHIKO  
*i* TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
*i* FILE REFERENCE: 030685-043  
*i* CURRENT APPLICATION NUMBER: US/10/932,182A  
*i* CURRENT FILING DATE: 2004-09-02  
*i* NUMBER OF SEQ ID NOS: 197023  
*i* SOFTWARE: PatentIn version 3.3  
*i* SEQ ID NO: 2279  
*i* LENGTH: 366  
*i* TYPE: DNA  
*i* ORGANISM: *Saccharomyces pastorianus*  
US-10-932-182A-2279

Query Match 39.8%; Score 130; DB 7; Length 366;  
Best Local Similarity 68.0%; Pred. No. 2.6e-31;  
Matches 181; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Db 94 AAAAAGATTGGAGTAAATAATGACAGGGGCGCTGGGATATAGCC 153  
Qy 55 AAGAAGGCCCTTGAAAGTGAAGTAAAAAGTGGAAATCAGTAGCCCTCTGGGCTGGGATATTGTG 114  
Db 94 AAAAAGATTGGAGTAAATAATGACAGGGGCGCTGGGATATAGCC 153  
Qy 115 GTTGATAACTGTCCACITCGAGGAACACATTATGGATCTTGATAGATGTCAAGCT 174  
Db 154 GTTGACATCTGGCAATTGCAARACACATTAATGAAACCATTGATGGCATGCCCG 213  
Qy 175 AACCAACGGTGCCTGCAACTTCAGAAGTGTACTCTGCACTGGGACTCTGAACATGGTCAAGTGTG 234  
Db 214 AAGGTATGACGACAAGATAAACGATGTGGCATGGGTGTGAATAGCT 273  
Qy 235 TTTCACTTCCACTGCATCTCGCTGGCTCAAACACAGGCTGTCATTGGACAAAC 294  
Db 274 TTCCACTGGCAATTGCAATAATGGATCAAGACAGGAGATGGCATGCCGTGGACAAAC 333  
Qy 295 AGAGAGTGGGATTCAAAAAGTATGG 320  
Db 334 CAACCTTGGCAATTGGCAAGTGGCG 359

RESULT 6  
US-10-932-182A-2279  
*i* Sequence 2279, Application US/10932182A  
*i* Publication No. US200604625A1  
*i* GENERAL INFORMATION:  
*i* APPLICANT: NAKAO, YOSHIHIRO  
*i* APPLICANT: NAKAMURA, NORIHIRO SA  
*i* APPLICANT: KODAMA, YUKIKO  
*i* APPLICANT: FUJIMURA, TOMOKO  
*i* APPLICANT: ASHIKARI, TOSHIHIKO  
*i* TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
*i* FILE REFERENCE: 030685-043  
*i* CURRENT APPLICATION NUMBER: US/10/932,182A  
*i* CURRENT FILING DATE: 2004-09-02  
*i* NUMBER OF SEQ ID NOS: 197023  
*i* SOFTWARE: PatentIn version 3.3  
*i* SEQ ID NO: 2279  
*i* LENGTH: 366  
*i* TYPE: DNA  
*i* ORGANISM: *Saccharomyces pastorianus*  
US-10-932-182A-2279

Query Match 39.8%; Score 130; DB 7; Length 366;  
Best Local Similarity 68.0%; Pred. No. 2.6e-31;  
Matches 181; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Db 94 AAAAAGATTGGAGTAAATAATGACAGGGGCGCTGGGATATAGCC 153  
Qy 55 AAGAAGGCCCTTGAAAGTGAAGTAAAAAGTGGAAATCAGTAGCCCTCTGGGCTGGGATATTGTG 114  
Db 94 AAAAAGATTGGAGTAAATAATGACAGGGGCGCTGGGATATAGCC 153  
Qy 115 GTTGATAACTGTCCACITCGAGGAACACATTATGGATCTTGATAGATGTCAAGCT 174  
Db 154 GTTGACATCTGGCAATTGCAARACACATTAATGAAACCATTGATGGCATGCCCG 213  
Qy 175 AACCAACGGTGCCTGCAACTTCAGAAGTGTACTCTGCACTGGGACTCTGAACATGGTCAAGTGTG 234  
Db 214 AAGGTATGACGACAAGATAAACGATGTGGCATGGGTGTGAATAGCT 273  
Qy 235 TTTCACTTCCACTGCATCTCGCTGGCTCAAACACAGGCTGTCATTGGACAAAC 294  
Db 274 TTCCACTGGCAATTGCAATAATGGATCAAGACAGGAGATGGCATGCCGTGGACAAAC 333  
Qy 295 AGAGAGTGGGATTCAAAAAGTATGG 320  
Db 334 CAACCTTGGCAATTGGCAAGTGGCG 359

RESULT 7  
US-10-932-182A-78459  
*i* Sequence 78459, Application US/10932182A  
*i* Publication No. US200604625A1  
*i* GENERAL INFORMATION:  
*i* APPLICANT: NAKAO, YOSHIHIRO  
*i* APPLICANT: NAKAMURA, NORIHIRO  
*i* APPLICANT: KODAMA, YUKIKO  
*i* APPLICANT: FUJIMURA, TOMOKO  
*i* APPLICANT: ASHIKARI, TOSHIHIKO  
*i* TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
*i* FILE REFERENCE: 030685-043  
*i* CURRENT APPLICATION NUMBER: US/10/932,182A  
*i* CURRENT FILING DATE: 2004-09-02  
*i* NUMBER OF SEQ ID NOS: 197023  
*i* SOFTWARE: PatentIn version 3.3  
*i* SEQ ID NO: 78459  
*i* LENGTH: 366  
*i* TYPE: DNA  
*i* ORGANISM: *Saccharomyces pastorianus*  
US-10-932-182A-78459

Query Match 37.8%; Score 123.6; DB 7; Length 366;  
Best Local Similarity 66.5%; Pred. No. 2.8e-29;  
Matches 177; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

Db 94 AAAAAGATTGGAGTAAATAATGACAGGGGCGCTGGGATATAGCC 153  
Qy 115 GTTGATAACTGTCCACITCGAGGAACACATTATGGATCTTGATAGATGTCAAGCT 174  
Db 154 GTTGACATCTGGCAATTGCAARACACATTAATGAAACCATTGATGGCATGCCCG 213  
Qy 175 AACCAACGGTGCCTGCAACTTCAGAAGTGTACTCTGCACTGGGACTCTGAACATGGTCAAGTGTG 234  
Db 214 AAGGTATGACGACAAGATAAACGATGTGGCATGGGTGTGAATAGCT 273  
Qy 235 TTTCACTTCCACTGCATCTCGCTGGCTCAAACACAGGCTGTCATTGGACAAAC 294  
Db 274 TTCCACTGGCAATTGCAATAATGGATCAAGACAGGAGATGGCATGCCGTGGACAAAC 333  
Qy 295 AGAGAGTGGGATTCAAAAAGTATGG 320  
Db 334 CAACCTTGGCAATTGGCAAGTGGCG 359

RESULT 8  
US-10-932-182A-78459  
*i* Sequence 78459, Application US/10932182A  
*i* Publication No. US200604625A1  
*i* GENERAL INFORMATION:  
*i* APPLICANT: NAKAO, YOSHIHIRO

APPLICANT: NAKAMURA, NORIHIKO  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TONOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 78459  
; LENGTH: 366  
; TYPE: DNA  
; ORGANISM: *Saccharomyces pastorianus*  
; US-10-932-182A-78459

Query Match 37.8%; Score 123.6; DB 7; Length 366;  
Best Local Similarity 65.5%; Pred. No. 2.8e-29; Indels 0; Gaps 0;  
Matches 177; Conservative 0; Mismatches 89;

QY 55 AAGAGCGCTTGAAGTGAANAACTGGATGCAACTAGGCCCTCGGCTGGGTATTTGTG 114  
Db 94 AAGAGAGATTGAAATTAGAACATGGACCGCATGGGTTTGGTCATGGGATATAGCT 153  
QY 115 GTTGATAACTGTGCCATCTGCAGAAACACATTATGGATCCTTCATAGAAATTCAACCT 174  
Db 154 GTTGACAATGTGTCTTGGACAAACATATGGACCATATGGACATTCATGGTCCAGCA 213  
QY 175 AACCAAGCCCTCGCTACTTCAGAAGAGGTACCTCGCATGGGAGTCTGTAAACCCT 234  
Db 214 AAGGCCATAGGGACACTATAATGAAATGGTGTGTAATCACCT 273  
QY 235 TTTCACTTCACTGATGATCTCGTGGCTAACACGACAGGTGTCATGGACAC 294  
Db 274 TTCCATTGACTGTATTAAATGGATCAAGAACGACCATGGCCATTAGATAAC 333  
QY 295 AGAGATGGGAATTCCAAGAATGATGG 320  
Db 334 CAACCTTGGAGTTAGCAAGATGGG 359

RESULT 9  
US-10-821-234-554  
; Sequence 554, Application US/10821234  
; Publication No. US20050255114A1  
; GENERAL INFORMATION:  
; APPLICANT: Labat, Ivan  
; APPLICANT: Stache-Crain, Birgit  
; APPLICANT: Andarmani, Susan  
; APPLICANT: Tang, Y. Tom  
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia  
; FILE REFERENCE: 821A  
; CURRENT APPLICATION NUMBER: US/10/821,234  
; PRIOR APPLICATION NUMBER: US 2003-04-07  
; CURRENT FILING DATE: 2004-04-07  
; NUMBER OF SEQ ID NOS: 1704  
; SOFTWARE: pt\_seq\_genes Version 1.0  
; SEQ ID NO: 554  
; LENGTH: 342  
; TYPE: DNA  
; ORGANISM: *Homo sapiens*  
; US-10-821-234-554

Query Match 23.2%; Score 76; DB 8; Length 342;  
Best Local Similarity 56.9%; Pred. No. 3.5e-14;  
Matches 164; Conservative 0; Mismatches 115; Indels 9; Gaps 1;

QY 26 CCCCGAGGGGACCAACAGCGCCGGCAAGAACGCCCTTGAAATGAAANCTGCAATG 85  
Db 50 CGGGAGCTCAGGCTCCAAAGTCGCAAGTCGCAAGATGTCCTCCCTCAAGAAGTCGAACG 109  
QY 86 CAGTAGCCCTGGGCTGGGATATGTGCAATCTGAGAACACCA 145

RESULT 10  
US-10-932-182A-81177/C  
; Sequence 81177, Application US/10932182A  
; Publication No. US20060046253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHIKO  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 81177  
; LENGTH: 153  
; TYPE: DNA  
; ORGANISM: *Saccharomyces pastorianus*  
; US-10-932-182A-81177

Query Match 22.6%; Score 74; DB 7; Length 153;  
Best Local Similarity 75.4%; Pred. No. 1.2e-13;  
Matches 92; Conservative 0; Mismatches 30; Indels 0; Gaps 0;

QY 55 AAGAGCGCTTGAAGTGAANAACTGGATGCAACTAGGCCCTCGGCTGGGTATTTGTG 114  
Db 128 AAGAGAGATTGAAATTAGAACATGGACCGCATGGGTTTGGTCATGGGATATAGCT 69  
QY 115 GTTGATAACTGTGCCATCTGCAGAAACACATTATGGATCCTTCATAGAAATTCAACCT 174  
Db 68 GTTGACAATGTGTATTGGACCATATGGAACTGATGGCAGTGAATGGAACTGATGGCAGCCA 9  
QY 175 AA 176  
Db 8 AA 7

RESULT 11  
US-10-932-182A-81177/C  
; Sequence 81177, Application US/10932182A  
; Publication No. US20060046253A1  
; GENERAL INFORMATION:  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; APPLICANT: NAKAMURA, NORIHIKO  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 81177  
; LENGTH: 153



APPLICANT: Brown, Eugene L.  
APPLICANT: Miller, Christopher P.  
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES RELATED TO OLIGONUCLEOTIDE ARRAYS  
TITLE OF INVENTION: TO MONITOR GENE EXPRESSION  
FILE REFERENCE: 01997-027701  
CURRENT APPLICATION NUMBER: US/11/128,061  
CURRENT FILING DATE: 2005-05-11  
PRIOR APPLICATION NUMBER: US 60/570,425  
PRIOR FILING DATE: 2004-05-11  
NUMBER OF SEQ ID NOS: 7285  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO: 2098  
LENGTH: 579  
TYPE: DNA  
ORGANISM: *Cricetulus griseus*  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (123)..(154)  
OTHER INFORMATION: n is a, c, g, or t  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: (547)..(568)  
OTHER INFORMATION: n is a, c, g, or t  
S-11-128-061-2098

RESULT 15  
S-11-128-049-2098  
Sequence 2098, Application US/11128049  
Publication No. US20060010513A1

GENERAL INFORMATION:

APPLICANT: Melville, Mark W.  
APPLICANT: Charlebois, Timothy S.  
APPLICANT: Mounts, William M.  
APPLICANT: Hann, Louane E.  
APPLICANT: Sincacore, Martin S.  
APPLICANT: Leonardi, Mark W.  
APPLICANT: Brown, Eugene L.  
APPLICANT: Miller, Christopher P.

TITLE OF INVENTION: OLIGONUCLEOTIDE ARRAYS TO MONITOR GENE EXPRESSION AND METHODS FOR  
MAKING AND USING SAME

FILE REFERENCE: 01997 027700

CURRENT APPLICATION NUMBER: US/11/128 , 049

CURRENT FILING DATE: 2005-05-11

PRIOR APPLICATION NUMBER: US 60/570 , 425

PRIOR FILING DATE: 2004-05-11

NUMBER OF SEQ ID NOS: 7285

SOFTWARE: Patentin version 3.3

SEQ ID NO: 2098

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OM nucleic - nucleic search, using sw model

Run on: March 8, 2006, 14:34:46 ; Search time 98.7354 Seconds  
(without alignments)  
5887.073 Million cell updates/sec

Title: US-09-541-462B-1  
Perfect score: 327  
Sequence: 1.atggccgatggatgt.....tccaaaaatggcactag 327

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1303057 seqs, 88780828 residues

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$  
Maximum Match 100\$  
Listing first 45 summaries

Database : Issued\_Patent\_NA:  
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2: /cgm2\_6/prodata/1/ina/5-COMB.seq:  
3: /cgm2\_6/prodata/1/ina/6-COMB.seq:  
4: /cgm2\_6/prodata/1/ina/6B-COMB.seq:  
5: /cgm2\_6/prodata/1/ina/H-COMB.seq:  
6: /cgm2\_6/prodata/1/ina/PCTUS-COMB.seq:  
7: /cgm2\_6/prodata/1/ina/PP-COMB.seq:  
8: /cgm2\_6/prodata/1/ina/RE-COMB.seq:  
9: /cgm2\_6/prodata/1/ina/backfile1.seq:  
\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1 - 999C-3894  
US-09-513-999C-3894  
/ Sequence 3894, Application US/09513999C  
/ Patent No. 6783961  
/ GENERAL INFORMATION:  
/ APPLICANT: Dumas Milne Edwards, J.B.  
/ ATTORNEY: Ducleir, A.  
/ APPLICANT: Giordano, J.Y.  
/ TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
/ Patent No. 6783961  
/ FILE REFERENCE: 59 US2 REG  
/ CURRENT APPLICATION NUMBER: US/09513,999C  
/ PRIORITY DATE: 2000-02-24  
/ PRIOR APPLICATION NUMBER: US 60/1122,487  
/ PRIOR FILING DATE: 1999-02-26  
/ NUMBER OF SEQ ID NOS: 36681  
/ SOFTWARE: Patent.pm  
/ SRQ ID NO: 3894  
/ LENGTH: 482  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION: 29..352  
/ FEATURE:  
/ NAME/KEY: misc\_feature  
/ LOCATION: 401  
/ OTHER INFORMATION: r=a or g  
/ FEATURE:  
/ NAME/KEY: misc\_feature  
/ LOCATION: 404  
/ OTHER INFORMATION: m=a or c  
US-09-513-999C-3894  
Query Match 100.0% ; Score 327; DB 3; Length 482;  
Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB	ID	Description
1	327	100.0	482	3	US-09-513-999C-3894	Sequence 3894, AP	Sequence 3894, AP
2	327	100.0	507	3	US-09-513-999C-3894	Sequence 4940, AP	Sequence 4940, AP
3	327	100.0	508	3	US-09-513-999C-3894	Sequence 3, Appli	Sequence 3, Appli
4	290.2	88.7	504	3	US-09-513-999C-3894	Sequence 5, Appli	Sequence 5, Appli
5	253.6	77.6	3208	3	US-09-513-999C-3894	Sequence 27, Appli	Sequence 27, Appli
6	253.6	77.6	3208	3	US-10-214-811-27	Sequence 27, Appli	Sequence 27, Appli
7	253.6	77.6	3208	3	US-10-766-074-27	Sequence 27, Appli	Sequence 27, Appli
8	170	52.0	402	3	US-09-513-999C-10371	Sequence 10371, A	Sequence 10371, A
9	170	52.0	463	3	US-09-621-976-15180	Sequence 15180, A	Sequence 15180, A
10	153.2	46.9	411	3	US-09-640-211A-1731	Sequence 1731, AP	Sequence 1731, AP
C 11	138.2	42.3	490	3	US-09-270-167-28812	Sequence 26812, A	Sequence 26812, A
C 12	138.2	42.3	1101	3	US-09-270-167-11265	Sequence 11265, A	Sequence 11265, A
C 13	123.6	37.8	480	3	US-09-914-324A-4	Sequence 4, Appli	Sequence 4, Appli
C 14	114.4	35.0	357	3	US-09-248-074-27	Sequence 5495, AP	Sequence 5495, AP
C 15	92.6	28.3	25274	3	US-09-621-976-16682	Sequence 16582, A	Sequence 16582, A
C 16	90	27.5	301	3	US-09-313-294A-492	Sequence 492, APPLI	Sequence 492, APPLI
C 17	74	22.6	342	3	US-09-826-312A-7	Sequence 7, Appli	Sequence 7, Appli
C 18	74	22.6	342	3	US-09-542-497A-7	Sequence 7, Appli	Sequence 7, Appli
C 19	74	22.6	342	3	US-10-10-767-7	Sequence 7, Appli	Sequence 7, Appli
C 20	46.4	14.2	439	3	US-09-799-551-296	Sequence 296, APPLI	Sequence 296, APPLI
C 21	36	11.0	601	3	US-09-949-016-174803	Sequence 174803, APPLI	Sequence 174803, APPLI
C 22	33.6	10.3	87734	3	US-09-17521-A	Sequence 17521, A	Sequence 17521, A
C 23	33.4	10.2	170	3	US-09-270-167-26253	Sequence 26253, A	Sequence 26253, A
C 24	33.4	10.2	585	3	US-09-270-167-10788	Sequence 10788, A	Sequence 10788, A

Db 149 AACTGTGCCATCTGAGGAACCACATTATGGATCAAGTCAACAG 208  
 Qy 181 GCGTCCGCTACTCTGAAAGGTGTACTGTGCATGGGAGTCATACTGGTTTAC 240  
 Db 209 GCGTCCGCTACTCTGAAAGGTGTACTGTGCATGGGAGTCATACTGGTTTAC 268  
 Db 241 TTCCACTGCACTCTGCTGCTAAAACAGCAGGTGTCCATGGCACACAGAG 300  
 Qy 269 TTCCACTGCACTCTGCTGCTGCTAAAACAGCAGGTGTCCATGGCACACAGAG 328  
 Db 301 TGGGAATCCAAAGTAGTGGCACTAG 327  
 Qy 329 TGGGAATCCAAAGTAGTGGCACTAG 355

RESULT 2  
 US-09-949-016-4940 Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; TITLE OF INVENTION: WITH HUMAN DISEASE,  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949, 016  
 ; CURRENT FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241, 755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237, 768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231, 498  
 ; PRIOR FILING DATE: 2000-09-08  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 4940  
 ; LENGTH: 507  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 ; US-09-949-016-4940

Query Match 100.0%; Score 327; DB 3; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Feature: ; Organism: Homo sapiens  
 Name/Key: CDS  
 Location: (7). (333)  
 Other Information: Rbx1  
 US-09-914-324A-3

Query Match 100.0%; Score 327; DB 3; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCAGCGATGGATGGATGGATACCCGAGGGCACAACCGGGCGGGAGAG 60

Db 7 ATGGCGCAGCGATGGATGGATGGATGGCTGGATATTGGTGTGTAT 120

Qy 61 CGCTTTGAAGTGAAGTGAAGTGGAACTGGAACTGGAACTGGAACTGGTGTGTAT 120

Db 67 CGCTTTGAAGTGAAGTGAAGTGGAACTGGAACTGGAACTGGTGTGTAT 126

RESULT 4  
 US-09-914-324A-5

Sequence 5, Application US/09914324A

Patent No. 6858709

GENERAL INFORMATION:

APPLICANT: Conway, Ronald C.

APPLICANT: Kamura, Takumi

APPLICANT: Oklamoma Medical Research Foundation

TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor

FILE REFERENCE: 021044-004600US

CURRENT APPLICATION NUMBER: US/09/914-324A

CURRENT FILING DATE: 2003-02-11

PRIOR APPLICATION NUMBER: US 60/121,787

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: WO PCT/US00/04838

RESULT 3  
 US-09-914-324A-3  
 Sequence 3, Application US/09914324A

Db 149 AACTGTGCCATCTGAGGAACCACATTATGGATCAAGTCAACAG 208  
 Qy 181 GCGTCCGCTACTCTGAAAGGTGTACTGTGCATGGGAGTCATACTGGTTTAC 240  
 Db 209 GCGTCCGCTACTCTGAAAGGTGTACTGTGCATGGGAGTCATACTGGTTTAC 268  
 Db 241 TTCCACTGCACTCTGCTGCTAAAACAGCAGGTGTCCATGGCACACAGAG 300  
 Qy 269 TTCCACTGCACTCTGCTGCTGCTAAAACAGCAGGTGTCCATGGCACACAGAG 328  
 Db 301 TGGGAATCCAAAGTAGTGGCACTAG 327  
 Qy 329 TGGGAATCCAAAGTAGTGGCACTAG 333

Query Match 100.0%; Score 327; DB 3; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Feature: ; Organism: Homo sapiens  
 Name/Key: CDS  
 Location: (7). (333)  
 Other Information: Rbx1  
 US-09-914-324A-3

Query Match 100.0%; Score 327; DB 3; Length 508;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-103;  
 Matches 327; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGGCGCAGCGATGGATGGATGGATACCCGAGGGCACAACCGGGCGGGAGAG 60

Db 7 ATGGCGCAGCGATGGATGGATGGATGGCTGGATATTGGTGTGTAT 120

Qy 61 CGCTTTGAAGTGAAGTGAAGTGGAACTGGAACTGGAACTGGTGTGTAT 120

Db 67 CGCTTTGAAGTGAAGTGAAGTGGAACTGGAACTGGAACTGGTGTGTAT 126

Qy 121 AACTGTGCCATCTGAGGAACCACATTATGGATCAAGTCAACAG 180

Db 127 AACTGTGCCATCTGAGGAACCACATTATGGATCAAGTCAACAG 186

Qy 121 AACTGTGCCATCTGAGGAACCACATTATGGATCAAGTCAACAG 186

Db 127 AACTGTGCCATCTGAGGAACCACATTATGGATCAAGTCAACAG 186

PRIOR FILING DATE: 2000-02-25  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: Patentin Ver. 2.1  
 SEQ ID NO: 5  
 LENGTH: 504  
 TYPE: DNA  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (18)..(344)  
 OTHER INFORMATION: Rbx1  
 US-09-914-324A-5

Query Match 88.7%; Score 290.2; DB 3; Length 504;  
 Best Local Similarity 93.0%; Pred. No. 2e-90;  
 Matches 304; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

Qy 1 ATGGCGCAGCGATGATGTGATAACCGGGCCAAAGAG 60  
 Db 18 ATGGCGCGGCCGATGGATGGATACCCCGGGCAACAGGGCGGGCAAGAG 77

RESULT 6  
 US-10-214-811-27  
 ; Sequence 27, Application US/10214811  
 ; Patent No. 6743621  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donohio, Gregory  
 ; APPLICANT: Scoville, John  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Friedrich, Glenn  
 ; APPLICANT: Abuin, Alejandro  
 ; APPLICANT: Zambowicz, Brian  
 ; APPLICANT: Sands, Arthur T.  
 ; TITLE OF INVENTION: No. 6743621 Human Proteases and  
 ; Polynucleotides Encoding the Same  
 ; FILE REFERENCE: LEX-0132-USA  
 ; CURRENT APPLICATION NUMBER: US/10/214,811  
 ; CURRENT FILING DATE: 2002-08-07  
 ; PRIORITY NUMBER: US/09/780,016  
 ; PRIORITY FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: US 60/181,294  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: Pasteseq for Windows Version 4.0  
 ; SEQ ID NO: 27

Query Match 77.6%; Score 253.6; DB 3; Length 3208;  
 Best Local Similarity 98.5%; Pred. No. 2.6e-77;  
 Matches 256; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 68 AAGTGAAGAACCAATTATGGATCTTGCAGAACCTGGATATTGTGGTGTG 120  
 Db 78 CGCTTGAACTTAAGTGAATGGATGGCTGGCACATTGTGGTGTG 137

Qy 121 AACGTGCCCATTCTGCAGAACCAATTATGGATCTTGCAGAACCTGGATATTGTGGTGTG 180  
 Db 138 AACGTGCCCATTCTGCAGAACCAATTATGGATCTTGCAGAACCTGGATATTGTGGTGTG 197

Qy 181 GCGTCGGCTACTTCGAGAAGTGTACTGTCGAGTGTCTGAACCATGGTTTAC 240  
 Db 198 GCGTCAGCTACTTCGAGAAGTGTACTGTCGAGTGTCTGAACCATGGTTTAC 257

Qy 241 TTCCCACTGCACTCTCGCTGCTCAAACAGACAGGTGTCATTGGACAACAGAG 300  
 Db 258 TTCCCACTGCACTCTCGCTGCTCAAACAGACAGGTGTCATTGGACAACAGAG 317

Qy 301 TGGGATTC2AAAGTATGGATGGCACTAG 327  
 Db 318 TGGGACTTCAGAACTATGGCCATTAG 344

RESULT 5  
 US-09-780-016-27  
 ; Sequence 27, Application US/09780016  
 ; Patent No. 6509456  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Donohio, Gregory  
 ; APPLICANT: Scoville, John  
 ; APPLICANT: Turner, C. Alexander Jr.  
 ; APPLICANT: Friedrich, Glenn  
 ; APPLICANT: Abuin, Alejandro  
 ; APPLICANT: Zambowicz, Brian  
 ; TITLE OF INVENTION: No. 6509456 Human Proteases and  
 ; Polynucleotides Encoding the Same  
 ; FILE REFERENCE: LEX-0132-USA  
 ; CURRENT APPLICATION NUMBER: US/09/780,016  
 ; CURRENT FILING DATE: 2001-02-09  
 ; PRIOR APPLICATION NUMBER: US 60/181,294  
 ; PRIOR FILING DATE: 2000-02-11  
 ; NUMBER OF SEQ ID NOS: 27  
 ; SOFTWARE: Pasteseq for Windows Version 4.0  
 ; SEQ ID NO: 27  
 ; LENGTH: 3208  
 ; TYPE: DNA  
 ; ORGANISM: homo sapiens  
 US-09-780-016-27

Query Match 77.6%; Score 253.6; DB 3; Length 3208;  
 Best Local Similarity 98.5%; Pred. No. 2.6e-77;  
 Matches 0; Mismatches 4; Indels 0; Gaps 0;

Qy 68 AAGTGAAGAACCAATTATGGATCTTGCAGAACCTGGATATTGTGGTGTG 120  
 Db 765 AAAAAGAAAAATGGATGGTGTCTGGCTGGATATTGTGGTGTG 2824

Qy 128 CCATCTGCAGAACCAATTATGGATCTTGCAGAACCTGGATATTGTGGTGTG 187  
 Db 2825 CCATCTGCAGAACCAATTATGGATCTTGCAGAACCTGGATATTGTGGTGTG 2884

Qy 188 CTACTTCAGAAAGTGTACTGTCGATGGGAGTGTGTAAACCATGGTTTCACTTCAC 247  
 Db 2885 CTACTTCAGAAAGTGTACTGTCGATGGGAGTGTGTAAACCATGGTTTCACTTCAC 2944

Qy 248 GCATCTCTCGCTGCTCAAACAGACAGGTGTCATTGGACAACAGAGTGGAAAT 307  
 Db 2945 GCATCTCTCGCTGCTCAAACAGACAGGTGTCATTGGACAACAGAGTGGAAAT 3004

Qy 308 TCCAAAAGTATGGCACTAG 327  
 Db 3005 TCCAAAAGTATGGCACTAG 3024

RESULT 7  
US-10-766-074-27  
Sequence 2<sup>7</sup>, Application US/10766074  
GENERAL INFORMATION:  
APPLICANT: Donoho, Gregory  
APPLICANT: Scoville, John C.  
APPLICANT: Turner, Alexander Jr.  
APPLICANT: Friedrich, Glenn  
APPLICANT: Abuin, Alejandro  
APPLICANT: Zambrowicz, Brian  
APPLICANT: Sands, Arthur T.  
TITLE OF INVENTION: Human Proteases and  
FILE REFERENCE: Polynucleotides Encoding the Same  
CURRENT APPLICATION NUMBER: US/10/766,074  
CURRENT FILING DATE: 2004-01-28  
PRIOR APPLICATION NUMBER: US/10/214,811  
PRIOR FILING DATE: 2002-08-07  
PRIOR APPLICATION NUMBER: US/09/780,016  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: US 60/181,294  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 27  
PRIOR FILING DATE: 2000-02-11  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: FastSEQ for Windows Version 4.0  
SEQ ID NO: 27  
LENGTH: 3208  
TYPE: DNA  
ORGANISM: homo sapiens  
US-10-766-074-27

Query Match 68 AGTGAATAGTGAATGGAACTGAGTAACCCCTGGGCTGGATATTCGGTTGATAACCTG 127  
Best Local Similarity 98.5%; Pred. No. 2.6e-77; Indels 0; Gaps 0;  
Matches 256; Conservative 0; Mismatches 4;

Query Match 68 AGTGAATAGTGAATGGAACTGAGTAACCCCTGGGCTGGATATTCGGTTGATAACCTG 127  
Best Local Similarity 98.5%; Pred. No. 2.6e-77; Indels 0; Gaps 0;  
Matches 256; Conservative 0; Mismatches 4;

RESULT 9  
US-09-611-976-15180  
Sequence 15180, Application US/09621976  
PATENT NO. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Robert S.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET 054 PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO: 15180  
LENGTH: 463  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: misc\_feature  
LOCATION: 74  
OTHER INFORMATION: n=a, g, c or t  
US-09-611-976-15180

Query Match 101 GCATAGAATGCACTAACCGGTCCGCTACTTCAGAGCTGACTGTCGATGGG 217  
Best Local Similarity 100.0%; Pred. No. 1.1e-48; Indels 0; Gaps 0;  
Matches 170; Conservative 0; Mismatches 0; Gaps 0;

Query Match 106 GCATAGAATGCACTAACCGGTCCGCTACTTCAGAGCTGACTGTCGATGGG 165  
Best Local Similarity 100.0%; Pred. No. 1.1e-48; Indels 0; Gaps 0;  
Matches 170; Conservative 0; Mismatches 0; Gaps 0;

Query Match 158 GCATAGAATGCACTAACCGGTCCGCTACTTCAGAGCTGACTGTCGATGGG 217  
Best Local Similarity 100.0%; Pred. No. 1.1e-48; Indels 0; Gaps 0;  
Matches 170; Conservative 0; Mismatches 0; Gaps 0;

Query Match 158 GCATAGAATGCACTAACCGGTCCGCTACTTCAGAGCTGACTGTCGATGGG 217  
Best Local Similarity 100.0%; Pred. No. 1.1e-48; Indels 0; Gaps 0;  
Matches 170; Conservative 0; Mismatches 0; Gaps 0;

Query Match 166 GAGCTGTAACCAGCTTCACTGCATCTGCTGAGCTCAAACGACAG 225  
Best Local Similarity 100.0%; Pred. No. 1.1e-48; Indels 0; Gaps 0;  
Matches 170; Conservative 0; Mismatches 0; Gaps 0;

Query Match 218 GAGCTGTAACCAGCTTCACTGCATCTGCTGAGCTCAAACGACAG 277  
Best Local Similarity 100.0%; Pred. No. 1.1e-48; Indels 0; Gaps 0;  
Matches 170; Conservative 0; Mismatches 0; Gaps 0;

Query Match 226 TGTCTCCATTGGACAAACGAGACTGGAAATTCCAAGACTATGGCCTAG 275  
Best Local Similarity 100.0%; Pred. No. 1.1e-48; Indels 0; Gaps 0;  
Matches 170; Conservative 0; Mismatches 0; Gaps 0;

Query Match 226 TGTCTCCATTGGACAAACGAGACTGGAAATTCCAAGACTATGGCCTAG 275  
Best Local Similarity 100.0%; Pred. No. 1.1e-48; Indels 0; Gaps 0;  
Matches 170; Conservative 0; Mismatches 0; Gaps 0;

RESULT 8  
US-09-513-999C-10371  
Sequence 10371, Application US/09513999C  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: Expression Tags and Encoded Human Proteins.  
PATENT NO. 6783961  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513, 999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122, 487  
PRIOR FILING DATE: 1999-02-26

Qy 278 TGTGTCATTGGACAAAGAGAGTGGGAATTCCAAAGTAGTGGCACTAG 327  
 Db 221 TGTGTCATTGGACAAAGAGAGTGGGAATTCCAAAGTAGTGGCACTAG 270

**RESULT 10**  
 US-09-640-211A-1731  
 Sequence 1731 Application US/09640211A  
 ; Patent No. 6833446

; GENERAL INFORMATION:  
 ; APPLICANT: Wood, Marion  
 ; APPLICANT: Shenk, Michael A.  
 ; APPLICANT: McGrath, Annette  
 ; APPLICANT: Glenn, Matthew  
 ; TITLE OF INVENTION: Compositions and Methods for the  
 ; FILE REFERENCE: 110000\_1021CU  
 ; CURRENT APPLICATION NUMBER: US/09/640,211A  
 ; CURRENT FILING DATE: 2000-08-16  
 ; NUMBER OF SEQ ID NOS: 2368  
 ; SOFTWARE: FastSEQ for Windows Version 4.0  
 ; SEQ ID NO: 1731  
 ; LENGTH: 411  
 ; TYPE: DNA  
 ; ORGANISM: Pinus radiata  
 ; FEATURE:  
 ; NAME/KEY: misc\_feature  
 ; LOCATION: (1) (411)  
 ; OTHER INFORMATION: n = A,T,C or G

US-09-640-211A-1731

Query Match 46.9%; Score 153.2; DB 3; Length 411;  
 Best Local Similarity 77.7%; Pred. No. 7e-43;  
 Matches 185; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Qy 58 AAGCGCTTTGAGTGAATAAGTGGAAATAGCAGTAGGCCCTCTGGCATGGATATTGGTT 117  
 Db 161 AACGTTTCGAATATCAGAACAGTGGAAATAGCAGTAGGCCCTTGCGTGGGATATTGGTT 220

Qy 118 GATAACTGTGCACATTCAGAACACATTATGGATTCTATGAAATGTCAACTAAC 177  
 Db 221 GATAATTGTGCACATTTCAGAACACATCATGGACCTCTATGTCAGGAAT 280

Qy 178 CAGGGCTTCGCTACTCACAGAACAGTGTACTGTGCATGGGAGTCTGTAACATGCTTT 237  
 Db 281 CAAGCAGTGCACAACAGTGTACTGTGCATGGGCTGTAACTCACGCCCTT 340

Qy 238 CACTTCACGTGATCTCGTGGCTAAACAGCAGAGGTGTGCCATTGACACAA 295  
 Db 341 CATTTCACATTGCTAAAGTCGGTGGCTAAAGCAGCAAGTGTGCCATTGATATA 398

Qy 49 CGGGCTAGAGCGCTTGAAGTGAATAAGTGGCACTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAAC 228  
 Db 322 CGAGGACGGGCGCTTGTGGTGAAGAAATGGGTGCGCACGCCATGTGGGATGGAC 263

Qy 109 ATTGTGGTTGATACTGTGCACATTGGATTTGTGATAGATGTT 168  
 Db 262 GTAGCAGTGGCAACTGTGCATTCGCGTACACATGCACTGTGATGGTGC 203

Qy 169 CAAGCTAACCGGGCTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAAC 228  
 Db 202 CGGGCGACCCGATGCAACAGTGTGCTGGGAGTGGAC 146

Qy 229 CATGCCTTCACTCCACTGCATCTCGCTGGCTAAACAGACAGGGAGTCTGCAATTG 288  
 Db 145 CACGCATTCACTTACACTGCATGGCGCTGGTGAAGAAACGGCTCTGTCCTG 86

Qy 289 GACAAAGAGAGTGGGAATTCCAAMGTGGCACTAG 327  
 Db 85 GACAAACAGAGTGGGTCTACCGAAGTACCGAAGTACCGCGCTAG 47

RESULT 12  
 US-09-270-767-11265/c  
 ; Sequence 11265 Application US/09270767  
 ; Patent No. 6703491  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Homburger et al.  
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*  
 ; FILE REFERENCE: File Reference: 7326-094  
 ; CURRENT APPLICATION NUMBER: US/09/270,767  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; CURRENT FILING DATE: 199-03-17  
 ; SEQ ID NO: 11265  
 ; LENGTH: 1101  
 ; TYPE: DNA  
 ; ORGANISM: *Drosophila melanogaster*  
 US-09-270-767-11265

Query Match 42.3%; Score 138.2; DB 3; Length 1101;  
 Best Local Similarity 71.0%; Pred. No. 1.9e-37;  
 Matches 198; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

Qy 49 GCGGGCTAGAGCGCTTGAAGTGAATAAGTGGCACTTCAGGCCCTCTGGCCTGGAT 108  
 Db 933 GCAGGACGGGCGCTTGTGGTGAAGAAATGGGTGCGCACGCCATGTGGGATGGAC 874

Qy 109 ATTGTGGTTGATACTGTGCACATTGGATTTGTGATAGATGTT 168  
 Db 873 GTAGCAGTGGCAACATGTGCCATTCCGTAACACATGATGAACTGTGATGGTGC 814

Qy 169 CAAGCTAACCGGGCTTCAGAGAGTGTACTGTGCATGGGAGTCTGTAAC 228  
 Db 813 CGGGCGACCCGATGCAACAGTGTGCTGGGAGTGGAC 757

Qy 229 CATGCCTTCACTCCACTGCATCTCGCTGGCTAAACAGACAGGGAGTCTGCAATTG 288

Db 756 CACGCATTCACTTACACTGCATGGCGCTGGTGAAGACGGCTCTGTCCTGCGCTG 697

Qy 289 GACAAAGAGAGTGGGAATTCCAAMGTGGCACTAG 327  
 Db 696 GACAAACAGAGTGGGTCTACCGAAGTACCGCGCTAG 658

RESULT 13  
 US-09-914-324A-4  
 ; Sequence 4, Application US/09914324A  
 ; Patent No. 6858709  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Conway, Joan A.  
 ; CURRENT APPLICATION: Conway, Joan A.  
 ; CURRENT FILING DATE: 1999-03-17  
 ; NUMBER OF SEQ ID NOS: 62517  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 26812  
 ; LENGTH: 490  
 ; TYPE: DNA  
 ; ORGANISM: *Drosophila melanogaster*

Query Match 42.3%; Score 138.2; DB 3; Length 490;  
 Best Local Similarity 71.0%; Pred. No. 1.2e-37;  
 Matches 198; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

APPLICANT: Oklahoma Medical Research Foundation  
 TITLE OF INVENTION: No. 6858709el Component of von Hippel-Lindau Tumor Suppressor Complex and Sce Ubiquitin Ligase  
 FILE REFERENCE: 02104-004600US  
 CURRENT APPLICATION NUMBER: US/09/914,324A  
 PRIOR APPLICATION NUMBER: US 60/121,787  
 PRIOR FILING DATE: 2003-02-11  
 PRIOR FILING DATE: 1999-02-26  
 PRIOR FILING DATE: 2000-02-25  
 NUMBER OF SEQ ID NOS: 12  
 SOFTWARE: Patentin ver. 2.1  
 SEQ ID NO: 4  
 LENGTH: 480  
 TYPE: DNA  
 ORGANISM: *Saccharomyces cerevisiae*  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: (4) . (369)  
 OTHER INFORMATION: Rbx1  
 US-09-914-324A-4

Query Match 37.8%; Score 123.6; DB 3; Length 480;  
 Best Local Similarity 66.5%; Pred. No. 1.4e-32;  
 Matches 177; Conservative 0; Mismatches 89; Indels 0; Gaps 0;  
 QY 55 AAGAAGCGCTTGAACTGAAAGTGGAAATGCACTGAGCTAGGCCCTGGCATATTGTG 114  
 Db 97 AAGAAGAATTGAATTAAGAACCTGGATTTGGTCAAGGGATAATGCT 156  
 QY 115 GTTGATAACTGTGCATCTCGAGAACACATTATGATCTTGGATAGATGTCAAGCT 174  
 Db 157 GTTGACAACGTGCTGATTTGGAGACATAATGAAACATTGAACTGGCC 216  
 QY 175 ACCCAGGGCTCGGTACTTCGAAAGAGTGTACTGTGGCATGGGATCTGTAACCATGCT 234  
 Db 217 AAGGCCATGAGGACACTGATAATGATGTGTAGCAGCTGGGTGTCAATAGCT 276  
 QY 235 TTTCACTTCAACTGCAATCTCGCTGGCTCAAATAAGACAGGTTGTGCATTTGGACAC 294  
 Db 277 TTCCATTGCACTGTATTAATGGATCAAGCAAGCAGCATGGCCATTAGATAAC 336  
 QY 295 AGAGAGTGGGAATTCCAAGGTATGG 320  
 Db 337 CAACCTTGGAGTTCAAGGTATGG 362

RESULT 14  
 US-09-248-796A-5495  
 Sequence 5495, Application US/09248796A.

Patent No. 674137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN

FILE REFERENCE: 107196.132

CURRENT FILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/096,796A

PRIOR FILING DATE: 1998-02-13

PRIOR APPLICATION NUMBER: US 60/096,409

PRIOR FILING DATE: 1998-08-13

SEQ ID NO: 5495

LENGTH: 357

TYPE: DNA

ORGANISM: *Candida albicans*

US-09-248-796A-5495

Query Match 35.0%; Score 114.4; DB 3; Length 357;  
 Best Local Similarity 66.8%; Pred. No. 1.9e-29;  
 Matches 179; Conservative 0; Mismatches 86; Indels 3; Gaps 1;

Qy 62 GCTTGTAAAGTGGAAATGCACTAGCCCTCTGGGCTGGATATTGGTTGATA 121.  
 Db 89 GATTTGAACTGAAARATGGCAACATGGCTTTGTCATGGCAAAATGGAAA 148  
 Qy 122 ACTGTGCCATCTGGAGGACCACTTATGGATCTTGCATAGATGTCAAGCTAA---CC 178  
 Db 149 ATTTGCCCCATTTGAGAAATCATTAATGGAAACCATGTTGATGTCAACCAATGCTA 208  
 Qy 179 AGGGTCCGCTACTTCAGAAGACTGTAATGCTGAGCTGGGAGATCTGTAAACCACATCTTTC 238  
 Db 209 TGGGTAATATTCCCTCAGAGAGTGTATTCGGGAGATGTATCATCATTC 268  
 Qy 239 ACTTCACTGCACTGATCTCCCTGGCTCAAACACACAGCTGTCCATTGGACAGAG 298  
 Db 269 ATTACATGTTATAGAATGTTGAAACAAATCATGTCCTTGGATTTGATA 328  
 Qy 299 AGTGGAAATTCCAAAGTATGGCACTA 326  
 Db 329 ATTGGACTATCAAATGGTATTAA 356

RESULT 15  
 US-09-949-016-16682  
 Sequence 16682, Application US/09949016  
 Patent No. 6812339  
 GENERAL INFORMATION:  
 APPLICANT: VENTER, J. Craig et al.  
 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 FILE OF INVENTION: CL001307  
 CURRENT APPLICATION NUMBER: US/09/949,016  
 CURRENT FILING DATE: 2000-04-14  
 PRIORITY NUMBER: 60/241,755  
 PRIORITY FILING DATE: 2000-10-20  
 PRIORITY APPLICATION NUMBER: 60/237,768  
 PRIORITY FILING DATE: 2000-10-03  
 PRIORITY APPLICATION NUMBER: 60/231,498  
 PRIORITY FILING DATE: 2000-09-08  
 NUMBER OF SEQ ID NOS: 20012  
 SOFTWARE: Fastseq for Windows Version 4.0  
 SEQ ID NO: 16682  
 LENGTH: 25274  
 TYPE: DNA  
 ORGANISM: Human  
 US-09-949-016-16682

Query Match 28.3%; Score 92.6; DB 3; Length 25274;  
 Best Local Similarity 96.0%; Pred. No. 6.1e-21;  
 Matches 95; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 221 TCTCTTAACCATGCTTTTCACTTTCACGTGATCTCGCTGGCTCAAACACGACAGGTGT 280  
 Db 18403 TCTTTCAGCTGCTTTCACTTCACGTGATCTCGCTGGCTCAAACACGACAGGTGT 18462  
 Qy 281 GTCATTTGGACAAAGAGTGGGAATTCCAAGATG 319  
 Db 18463 GTCTATTTGGACAAAGAGTGGGAATTCCAAGATG 18501

Search completed: March 8, 2006, 14:48:17  
 Job time : 100.735 secs